

F;233-485/Domain: protein kinase homology <KIN>
F;241-249/Region: protein kinase ATP-binding motif

Query Match 100.0%; Score 2571; DB 2; Length 507;

Best Local Similarity 100.0%; Pred. No. 1; Gaps 118;

Matches 507; Conservative 0; Mismatches 18; Indels 14; Gaps 2;

Qy 1 MAGRSLSVSRRAFGCDSAAELPRVSPRLRAWHPPV/SARMPTTRWADGTCITKCENT 60

Db 1 MAGRSLSVSRRAFGCDSAAELPRVSPRLRAWHPPV/SARMPTTRWAPGTCITKCENT 60

Qy 1 MAGRSLSVSRRAFGCDSAAELPRVSPRLRAWHPPV/SARMPTTRWADGTCITKCENT 60

Db 1 MAGRSLSVSRRAFGCDSAAELPRVSPRLRAWHPPV/SARMPTTRWAPGTCITKCENT 60

Qy 1 MAGRSLSVSRRAFGCDSAAELPRVSPRLRAWHPPV/SARMPTTRWADGTCITKCENT 60

Db 1 MAGRSLSVSRRAFGCDSAAELPRVSPRLRAWHPPV/SARMPTTRWADGTCITKCENT 60

RESULT 2

A49865 protein-tyrosine kinase (EC 2.7.1.112) matk, long splice form - human

N;Alternate names: hematopoietic consensus tyrosine-lacking (HNL) non-receptor tyrosine

C;Species: Homo sapiens (man) #sequence_revision 30-Jun-1995 #text_change 26-May-2000

C;Accession: A49865; Cited: 30-Jun-1995 #sequence_revision 30-Jun-1995 #text_change 26-May-2000

R;Bennett, B.D.; Cowley, S.; Jiang, S.; London, R.; Deng, B.; Grabarek, J.; Groopman, J.

J. Biol. Chem., 269, 1088-1074, 1994

A;Title: Identification and characterization of a novel tyrosine kinase from megakaryocytes

A;Reference number: A49865; MUID:94117408; PMID:8286563

A;Accession: A49865; Status: preliminary; Residues: 1-527 <BEN>

A;Molecule type: mRNA

A;Cross-references: GDB:MATK; lsk: GDB:304667

A;Map position: 19p13.3-19p13.3

A;Cross-references: For an alternative splice form, see PIR: A55625.

C;Genetics: A;Cross-references: GB:L118974; NID:945449; PIDN:AAA16703.1; PID:9459550

A;Gene: GDB:MATK; lsk: GDB:304667

A;Cross-references: GDB:MATK; lsk: GDB:304667

A;Map position: 19p13.3-19p13.3

A;Cross-references: For an alternative splice form, see PIR: A55625.

C;Genetics: A;Cross-references: GB:L118974; NID:945449; PIDN:AAA16703.1; PID:9459550

A;Gene: GDB:MATK; lsk: GDB:304667

A;Cross-references: GDB:MATK; lsk: GDB:304667

A;Map position: 19p13.3-19p13.3

RESULT 3

159296 protein-tyrosine kinase (EC 2.7.1.112), megakaryocyte-associated - mouse

N;Alternate names: ctk

C;Species: Mus musculus (house mouse)

C;Accession: I59296; I58407; B55225; I49621

R;Chow, D.M.L.; Jarvis, C.D.; Hu, O.; Nye, S.H.; Gervais, F.G.; Veillette, A.; Matis, M.

Proc. Natl. Acad. Sci. U.S.A., 91, 4975-4979, 1994

A;Title: Ntk, a csk-related protein-tyrosine kinase expressed in brain and T lymphocytes

A;Reference number: I59296; MUID:94255451; PMID:8197166

A;Status: preliminary; translated from GB/EMBL/DDJB

A;Molecule type: mRNA

A;Residues: 1-505 <RES>

A;Cross-references: GB:L27738; NID:9507289; PIDN: AAB59677.1; PID:9507290

R;Chow, D.M.; Davidson, D.; Fournel, M.; Gosselin, P.; Lemieux, S.; Lyu, M.S.; Kozak, Oncogene, 9, 3437-3448, 1994

A;Title: Two distinct protein isoforms are encoded by ntk, a csk-related tyrosine pro

A;Reference number: I58407; MUID:95060800; PMID:7970703

A;Accession: I58407; Status: preliminary; Residues: 1-505 <RES>

A;Molecule type: DNA

A;Cross-references: GB:L33339; NID:9609536; PIDN: AAB64431.1; PID:9609537

C;Keywords: alternative splicing; ATP; phosphotransferase; tyrosine-specific protein kin

F;55-105/Domain: SH3 homology <SH3>

F;123-211/Domain: SH2 homology <SH2>

F;33-484/Domain: protein kinase homology <KIN>

F;241-249/Region: protein kinase ATP-binding motif

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: mRNA

A; Residues: 41-505 <VR>
 R; Kaneko, Y.; Nonoguchi, K.; Fukuyama, H.; Takano, S.; Higashitsuji, H.; Nishiyama, H.; Oncogene 10, 945-952, 1995
 A; Title: Presence of alternative 5' untranslated sequences and identification of cells expressing the human *SH2B1* gene
 A; Reference number: 149621; MUID:95206787; PMID:7898936
 A; Status: translated from GB/EMBL/DBJ
 A; Molecule type: mRNA
 A; Residues: 41-505 <VR3>
 A; Cross-references: GB;L34542; NID:9530157; PID:9530158
 A; Genetics:
 C; Superfamily: batk
 C; Subfamily: protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH3 homology
 C; Keywords: ATP; phosphotransferase; tyrosine-specific protein kinase
 F; 14-64/Domain: SH3 homology <SH3>
 F; 81-170/Domain: SH2 homology <SH2>
 F; 122-445/Domain: protein kinase homology <KIN>
 F; 199-207/Region: protein kinase ATP-binding motif
 A; Gene: Ntk; P56ntk
 A; Introns: 23/3
 C; Superfamily: protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH3 homology
 C; Keywords: ATP; phosphotransferase; tyrosine-specific protein kinase
 F; 53-107/Domain: SH3 homology <SH3>
 F; 120-209/Domain: SH2 homology <SH2>
 F; 239-247/Region: protein kinase ATP-binding motif
 Query Match 87.6%; Score 2341; DB 2; Length 505;
 Best Local Similarity 87.4%; Pred. No. 3.7e-113; Matches 443; Conservative 27; Mismatches 35; Indels 2; Gaps 2;
 Qy 1 MAGRGLSVLWWRFHGGCDSAEELPRVSPRFLRAWHPPPSARMTRWRWAPGTCITKCERT 60
 Db 1 MARRSSRVSMWLFEGWES-RDLPVSPRLFGAWHPRAPAARMET-RWAPGTCITKCENS 58
 Qy 61 RPKPGELAFRKGDVVTILEACENSKSWRKHKHSGQEGSLLAACAREREALSDPKUSLM 120
 Db 59 RPKPGELAFRKGDVVTILEACEDSKSWTRAKHKHSGQEGSLLAACAROREALSDPKUSLM 118
 Qy 121 PRFHGKTSQGAEAVQQLQPPEDGLFLVRESARHPGDYVLCVS 180
 Db 119 PRFHGKTSQGAEAVQQLQPPEDGLFLVRESARHPGDYVLCVS 178
 Qy 181 DAEVFCNLMDKVEHYSKDKGATCTKLVRPKRKHGTSAAEELARAGWLNLNQHLOHITLGQ 240
 Db 179 DAEVFCNLMDKVEHYSKDKGATCTKLVRPKRKHGTSAAEELARAGWLNLNQHLOHITLGQ 238
 Qy 241 IGEGEFGAVLQSGRYLQGOKVAVNIKCDYTAQFLDEAVTMTKHOHENVYRLQGVLHQL 300
 Db 239 IGEGEFGAVLQGFLGQKVAVNIKCDYTAQFLDEAVTMTKQHRLNVLRLQGVLHQL 298
 Qy 301 YIVMEHYSKGNLVNFRLRGRALVNTQLQFSLHVAEGMELYESKLLVHDLAARNLIV 360
 Db 299 YIVMEHYSKGNLVNFRLRGRALVNTQLQFSLHVAEGMELYESKLLVHDLAARNLIV 358
 Qy 361 SEDLVAKVSDFGIKAERKGGLDSSRLPKWVTAPEALKKGKFTSKDWSFGVLLWEVTSY 420
 Db 359 SEDLVAKVSDFGIKAERKGGLDSSRLPKWVTAPEALKKGKFTSKDWSFGVLLWEVTSY 418
 Qy 421 GRAPYKMSLKEVSEAYEVKGYRMEPPEGCPGPVHMLMSCWELAEPARPERKLAKLAR 480
 Db 419 GRAPYKMSLKEVSEAYEVKGYRMEPPEGCPGPVHMLMSCWELAEPARPERKLAKLAR 478
 Qy 481 ELSRAGAPASVSGQDAGTSRPSQEP 507
 Db 479 ELSRAGAPASVSGQDAGTSRPSQEP 505
 RESULT 4
 156579 protein-tyrosine kinase (EC 2.7.1.112) batk - rat
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 04-Mar-2000
 C;Accession: 156579
 A; Reference number: 156579; MUID:95106341; PMID:7807586
 A; Accession: I56579
 A; Status: preliminary; translated from GB/EMBL/DBJ
 A; Molecule type: mRNA
 A; Residues: 1-465 <RES>
 A; Cross-references: EMBL:005210; NID:9450232; PIDN:AAA18829; 1; PID:9450233
 A; Genetics:
 C; Superfamily: protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH3 homology
 C; Keywords: ATP; phosphotransferase; tyrosine-specific protein kinase
 F; 13-63/Domain: SH3 homology <SH3>
 F; 80-169/Domain: SH2 homology <SH2>
 F; 191-443/Domain: protein kinase homology <KIN>
 F; 199-207/Region: protein kinase ATP-binding motif
 Query Match 82.7%; Score 2209; DB 2; Length 465;
 Best Local Similarity 89.3%; Pred. No. 4.5e-107; Matches 417; Conservative 27; Mismatches 22; Indels 1; Gaps 1;
 Qy 42 NPTRRWAPGTCITKCCEHTRPKGELAFRKDVVTILEACENSKSWRKHKHSGQEGSLLA 101
 Db 1 NPTQRWAPGTCITKCCEHTRPKGELAFRKDVVTILEACEDSKSWTRAKHKHSGQEGSLLA 60
 Qy 162 FGRDVTHYRVIHGDHILTIDEAVFCNLMDKVEHYSKDKGAICTKLVRPKRKHGTSAAE 221
 Db 121 FGRDVTHYRVIHGDHILTIDEAVFCNLMDKVEHYSKDKGAICTKLVRPKRKHGTSAAE 180
 Qy 222 ELARAGWLNQHOLTGAGTQEGEGEGAVLQGFLYLGOKVAVNIKCDYTAQFLDEAVMT 281
 Db 181 ELAKACWLQDLOQHLTGAQIEGEGEGAVLQGFLYLGOKVAVNIKCDYTAQFLDEAVMT 240
 Qy 282 KMQHENLYRLGVLHQGLYVMEHYSKGNLVNFRLRGRALVNTQLQFSLHVAEGMELYESKLLVHDLAARNLIV 341
 Db 241 KLOHRNLVRLGVLHQGLYVMEHYSKGNLVNFRLRGRALVNTQLQFSLHVAEGMELYESKLLVHDLAARNLIV 300
 Qy 342 YLESKKLVHDLAARNLIVLSDLVAKVSDFLAKAE-RKGIDSSRLPKWVTAPEALKHGK 400
 Db 301 YLESKKLVHDLAARNLIVLSDLVAKVSDFLAKAE-RKGIDSSRLPKWVTAPEALKHGK 360
 Qy 401 FTISKSYWPSRFLWVWFSYKRAYPAKMSLKEVSEAEVKGKMRMEPPEGCPGPVHMLSSC 460
 Db 361 FSSKSYWPSRFLWVWFSYKRAYPAKMSLKEVSEAEVKGKMRMEPPEGCPGPVHMLSSC 420
 Qy 461 WEAEPARRPPRPLKAKLARSLSAGAPASVSGQDAGTSRPSQEP 507
 Db 421 WEAEPSSRPPRPLKAKLARSLSAGAPASVSGQDAGTSRPSQEP 467
 RESULT 5
 148226 protein-tyrosine kinase (EC 2.7.1.112) Ctk - mouse
 C; Alternative names: csk-type protein-tyrosine kinase
 C; Species: Mus musculus (house mouse)
 C; Date: 15-Mar-1996 #sequence_revision 15-Mar-1996 #text_change 04-Feb-2000
 C; Accession: 148926
 R; Kiges, S.; Adam, D.; Class, K.; Farnoli, J.; Bolen, J.B.; Penhallow, R.C.
 Proc. Natl. Acad. Sci. U.S.A. 91, 2597-2601, 1994
 A; Title: Ctk: a protein-tyrosine kinase related to Csk that defines an enzyme family
 A; Reference number: A53469; MUID:94195789; PMID:7511815
 A; Accession: I48926
 A; Status: preliminary
 A; Molecule type: mRNA
 A; Residues: 1-465 <RES>
 A; Cross-references: EMBL:005210; NID:9450232; PIDN:AAA18829; 1; PID:9450233
 A; Genetics:
 C; Superfamily: protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH3 homology
 C; Keywords: ATP; phosphotransferase; tyrosine-specific protein kinase
 F; 13-63/Domain: SH3 homology <SH3>
 F; 80-169/Domain: SH2 homology <SH2>
 F; 191-443/Domain: protein kinase homology <KIN>
 F; 199-207/Region: protein kinase ATP-binding motif

Best Local Similarity 89.5%; Pred. No. 1.9e-105; Matches 417; Conservative 23; Mismatches 25; Indels 1; Gaps 1; Db 127 EHRIIISSSKL SIDEVYFENL MOLV EHYTTAD GLCS RLKPKW MEGTvaQDFRSRS 186

Qy 42 MPTRRWAPOTQCITKCHPCKGELARKRGDV TILEACEN SWYRKH TSQEGILLA 101

Db 1 MPT-RWAQCTQCMKCE SPKGE LAFRKG DV TILACEN SWYRKH TSQEGILLA 59

Qy 102 AGALREREA LADSADPKLSLMPWFKKIS GOAVQOLQ PFDGLF LVR ERSARH PEGDYVLCWS 161

Db 60 AAALRHRGEA LSTPKLSLMPWFKKIS GOAVQOLQ PFDGLF LVR ERSARH PEGDYVLCWS 119

Qy 162 FGRDVTHYV LHRDGH LTIDEA VFCNLM DMV EY SKRKGATCTKLYF KRGITKSAEE 221

Db 120 FGRDVTHYV LHRDGH LTIDEA VFCNLM DMV EY SKRKGATCTKLYF KRGITKSAEE 179

Qy 222 ELARAGW LNLQH LTGLGAGIG EGF GAVI QGEYLGOKVAKN KCDVTAQAF DETA WT 281

Db 180 ELARAGW LNLQH LTGLGAGIG EGF GAVI QGEYLGOKVAKN KCDVTAQAF DETA WT 239

Qy 282 KMOHENL VRLGV LHLQGKIVM EHVSKGNL VNLFL RTGR ALVNTA QLQ FSLHVAEGM 341

Db 240 KLOHNL VYLLGV LHLQGKIVM EHVSKGNL VNLFL RTGR ALVNTA QLQ FSLHVAEGM 299

Qy 342 YLESKKL VLRD LARNTL VSED LVA KERKG DSSRLPV KWT APEALKHGF 401

Db 300 YLESKKL VLRD LARNTL VSED LVA KERKG DSSRLPV KWT APEALKHGF 359

Qy 402 TSKD VDW SGV LWEVFSY GRAPK PMSK IVE AV EK VY RMR PEGC PGPV ULMSCW 461

Db 360 SS KSD VDW SGV LWEVFSY GRAPK PMSK IVE AV EK VY RMR PEGC PGPV ULMSCW 419

Qy 462 EAEP ARPPPF KLA EK LARL SAGA PVS GODA GS SPSR S0EP 507

Db 420 EAEP ARPPPF KLA EK LARL SAGA PVS GODA GS SPSR S0EP 465

RESULT 6 .

A1:973

protein-tyrosine kinase (EC 2.7.1.112) CSK - chicken (fragment)

C:Species: Gallus gallus (chicken)

C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 18-Jun-1999

C:Accession: A1:973

R;Sabe, H.; Knudsen, B.; Okada, M.; Nada, S.; Nakagawa, H.; Hanafusa, H.

Proc. Natl. Acad. Sci. U.S.A. 89, 2190-2194, 1992

A;Title: Molecular cloning and expression of chicken C-terminal Src kinase: lack of stat

A;Reference number: A1:973; MUID:92196083; PMID:1372437

A;Accession: A1:973

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-450 <SAB>

A;Cross-references: GB:M85039; NID:9212701; PIDN:AAA51436.1; PID:9212702

A;Note: sequence extracted from NCBI backbone (NCBINR88058, NCBIPI:88059)

C:Superfamily: protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH3 homology; ATP; autophosphorylation; phosphoprotein; phosphotransferase; tyrosine-specific

F;16-65;Domain: SH3 homology <SH3>

F;16-171;Domain: SH2 homology <SH2>

F;193-47/Domain: protein kinase homology <KIN>

F;201-209/Region: protein kinase Atp-binding motif

Query Match 46.9%; Score 1253.5; DB 2; Length 450; Best Local Similarity 53.9%; Pred. No. 1.8e-57; Matches 234; Conservative 84; Mismatches 113; Indels 3; Gaps 2; Db 47 WAPGTCITKCEHTRPKPGE LAFRKG DV TILACEN SWYRKH TSQEGILLA 106

Db 8 WPSCTECAKYNHGTQADQPLPSKG DYLITAVK PPNWYKAKN KV GREGI PANYWQ 66

Qy 107 EREALSADPKLSLMPWFKKIS GOAVQOLQ PFDGLF LVR ERSARH PEGDYVLCWS 166

Db 67 KREGV KAGKL SLM PWF HFKITR QEA RLLY PPTGFL VRE STN PGP DYT GLVCS CEGKV 126

Qy 167 IHYVTHRGH LTIDEA VFCNLM DMV EY SKRKGATCTKLYF KRGITKSAEE 226

A;Introns: 5/3; 43/3; 81/2; 154/3; 186/1; 208/1; 241/2; 271/3; 296/2; 361/3; 390/3

Db 127 EHRIIISSSKL SIDEVYFENL MOLV EHYTTAD GLCS RLKPKW MEGTvaQDFRSRS 186

Qy 227 GWLNLQHITGQOIGECEFGAVLQGEYLGQVAKN KCDVTAQAF DETA WT AMVTHO 286

Db 187 GWALNLQHITGQOIGECEFGAVLQGEYLGQVAKN KCDVTAQAF DETA WT ASWMTQLRHS 246

Qy 287 NLVRLGILHQ -GLIT- MEHVSKGNL VNLFL RTGR ALVNTA QLQ FSLHVAEGM EYLE 344

Db 247 NLVQLGVIVE EK VY RMR PEGC PGPV ULMSCW 306

Qy 345 SKKLVH RDLA RNTL VSED LVA KERKG DSSRLPV KWT APEALKHGF 404

Db 307 ANNEVH RDLA RNLV NLSE DIAK VSDC DLT K EASST QDTG KLPV KWT APEALKHGF EYSTK 366

Qy 405 SDW SFG YLW EYFSY GRAPK PMSK IVE AV EK VY RMR PEGC PGPV ULMSCW 464

Db 367 SDW SFG YLW EYFSY GRAPK PMSK IVE AV EK VY RMR PEGC PGPV ULMSCW 426

Qy 465 PARRPF KLA EK LARL SAGA PVS GODA GS SPSR S0EP 478

Db 427 PGH RPSF HOLEQ L 440

RESULT 7 .

JH0559

protein-tyrosine kinase (EC 2.7.1.112) CSK - human

N;Alternate names: protein-tyrosine kinase cyl; protein-tyrosine kinase T2

C:Species: Homo sapiens (man)

C:Date: 30-Jun-1992 #sequence_revision 20-Aug-1994 #text_change 21-Jul-2000

C:Accession: JH0559; S38818; S19024; S19025

R;Braeuninger, A.; Holtrich, U.; Strebhardt, K.; Ruebsamen-Waigmann, H.

Gene 110, 205-211, 1992

A;Title: Isolation and characterization of a human gene that encodes a new subclass of

A;Reference number: S38818; MUID:93241739; PMID:7683131

A;Reference number: JH0559; MUID:92165060; PMID:1371489

A;Accession: JH0559

A;Molecule type: mRNA

A;Residues: 1-450 <BRA>

A;Cross-references: EMBL:X59932; NID:930255; PIDN:CAA42556.1; PID:930256

A;Experimental source: Lung

R;Braeuninger, A.; Kurn, T.; Strebhardt, K.; Ruebsamen-Waigmann, H.

Oncogene 8, 1365-1369, 1993

A;Title: Characterization of the human CSK locus.

R;Braeuninger, A.; Holtrich, U.; Strebhardt, K.; Ruebsamen-Waigmann, H.

Gene 110, 205-211, 1992

A;Title: Isolation and characterization of a human gene that encodes a new subclass of

A;Reference number: S38818; MUID:93241739; PMID:7683131

A;Accession: S38818

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-450 <BRA>

A;Cross-references: EMBL:X74765; NID:9402582; PIDN:CA B59562.1; PID:96077093

R;Partanen, J.; Armstrong, E.; Bergman, M.; Maekelae, T.P.; Hirvonen, H.; Huebner, K.

Oncogene 6, 2013-18, 1991

A;Title: cty encodes a putative cytoplasmic tyrosine kinase lacking the conserved tyr

A;Reference number: S19024; MUID:92050797; PMID:1945408

A;Accession: S19024

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-450 <PAR>

A;Cross-references: EMBL:X60114; NID:930314; PIDN:CAA42713.1; PID:930315

R;Holtrich, U.; Braeuninger, A.; Strebhardt, K.; Ruebsamen-Waigmann, H.

Proc. Natl. Acad. Sci. U.S.A. 88, 10411-10415, 1991

A;Title: Two additional protein-tyrosine kinases expressed in human lung: fourth memb

A;Reference number: S19025; MUID:92073297; PMID:1720539

A;Accession: S19025

A;Cross-references: EMBL:X59932; NID:930255; PIDN:CAA42556.1; PID:930256

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: mRNA

A;Residues: 1-450 <HOL>

A;Cross-references: EMBL:X59932; NID:930255; PIDN:CAA42556.1; PID:930256

A;Note: this sequence was submitted to the EMBL Data Library, June 1991

C:Comment: This protein lacks the N-myristylation and autophosphorylation sites present

C:Genetics:

A;Gene: GDB:CSK

A;Cross-references: GDB:131642; OMIM:124095

C;Function:

A;Description: catalyzes the phosphorylation of a peptidyl tyrosine residue by ATP

C;Superfamily: protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH3 homology

C;Keywords: ATP; phosphotransferase; tyrosine-specific protein kinase

F;16-65/Domain: SH3 homology <SH3>

F;82-171/Domain: SH2 homology <SH2>

F;193-447/Domain: protein kinase homology <KIN>

F;201-209/Region: protein kinase ATP-binding motif

F;222/Active site: Lys #status predicted

Query Match 46 5%; Score 1245.5; DB 1; Length 450;

Best Local Similarity 54.1%; Pred. No. 4.6e-57; Matches 235; Conservative 81; Mismatches 115; Indels 3; Gaps 2;

Qy 47 WAPGTOCTKCTRTPKGELAFRKGDWVTLAEACENKSMYRVIKHTSGOEGLLAGALR 106

Db 8 WPSGTECIAKYNFHGTAEQDLPFCKGKDVLTVAVTKDPNPKAKNPK-GREGIIPANYQ 66

Qy 107 BREALSADPKLISLMPWPHGKTSQGQAVQQLQPPDGLYRESARHPPGCVLCSVGRDV 166

Db 67 KREGVKGAKTSLMPWPHGKTRDQEAERLRLYPPGELYRESTNPGCVLSCDGKV 126

Qy 167 IHYRVIHRDGHLTIDEAVFFCNLMQDVHEVSKDKGAICTKLRVPRKRKHGTSAEELARA 226

Db 127 EHYRIMYHASKLISIDEEVYENLMLQVHEHTSDAGLCTRLIKPKVMEGIVAAQDEFYR 186

Qy 227 GWLLNQHLTGAGQEGEGAVLGEYLGQKVAKNIKDVTAQFLDTAVWTKMHE 286

Db 187 GWALNKKELKLQLQTGKGFDVMDYRGNKVAVCKIKNDATAQAFLAESVMTQLRHS 246

Qy 287 NLVRLLGVILHQ--GLYIVMEHVSQGNLVLNFRTRGALVNTAQJQFSLHVACMEYLE 344

Db 247 NLVOLQGVIVEEKGLYVTEYMAKGSLVYDYLRSRGSRVLAGDCLIKESDVCAMEYLE 306

Qy 345 SKKLVIRDLAARNLIVSLEDLVAKVSDFGGLAKAERKGDDSSRLPVIWTAPEALKHCKFTSK 404

Db 307 GNNFVHRLDAARNLIVSLEDNVAKVSDFGGLAKAERKGDDSSRLPVIWTAPEALKHCKFTSK 366

Qy 405 SDWWSFGVILWEVFSYGRAPYKPKMSLKEVSEAVKGYMRPEPPEGCPGPVHLMSSCWEAE 464

Db 367 SDWWSFGILWELMEIYSGRVPYPRFLKDVVPRVERGKYMADPDGCPPAVYEMKNCWHLQ 426

Qy 465 PARRPFKLAEKL 478

Db 427 AAMRPSFLQLEQL 440

RESULT 8

S15094 protein-tyrosine kinase (EC 2.7.1.112) CSK - rat

N;Alternate names: c-src kinase; tyro-13 kinase

C;Species: Rattus norvegicus (Norway rat)

C;Date: 30-Jun-1993 #sequence_change 30-Jun-1993 #text_change 11-Jun-1999

C;Accession: S15094; S18500; PT0195

R;Noda, S.; Obara, M.; MacAuley, A.; Cooper, J.A.; Nakagawa, H. Nature 351, 659-72, 1991. Cloning of a complementary DNA for a protein-tyrosine kinase that specifically

A;Title: Cloning of a complementary DNA for a protein-tyrosine kinase that specifically

A;Reference number: S15094; MUID:9126538; PMID:1709258

A;Accession: S15094

A;Molecule type: mRNA

A;Cross-references: EMBL:X58631; NID:957507; PIDN:CAA41484.1; PID:957508

A;Accession: S18500

A;Molecule type: protein

A;Cross-accession: PT0183; MUID:9122560; PMID:2025425

A;Molecule type: mRNA

A;Residues: 319-367 <LAI>

A;Experimental source: sciatic nerve

C;Genetics:

A;Gene: tyro-13

C;Superfamily: protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH3 homology

C;Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; tyrosine-specific protein kinase

F;16-65/Domain: SH3 homology <SH3>

F;82-171/Domain: SH2 homology <SH2>

F;193-447/Domain: protein kinase homology <KIN>

F;201-209/Region: protein kinase ATP-binding motif

F;222/Active site: Lys #status predicted

Query Match 46 5%; Score 1242.5; DB 1; Length 450;

Best Local Similarity 54.1%; Pred. No. 6.6e-57; Matches 235; Conservative 81; Mismatches 115; Indels 3; Gaps 2;

Qy 47 WAPGTOCTKCTRTPKGELAFRKGDWVTLAEACENKSMYRVIKHTSGOEGLLAGALR 106

Db 8 WPSGTECIAKYNFHGTAEQDLPFCKGKDVLTVAVTKDPNPKAKNPK-GREGIIPANYQ 66

Qy 107 BREALSADPKLISLMPWPHGKTSQGQAVQQLQPPDGLYRESARHPPGCVLCSVGRDV 166

Db 67 KREGVKGAKTSLMPWPHGKTRDQEAERLRLYPPGELYRESTNPGCVLSCDGKV 126

Qy 167 IHYRVIHRDGHLTIDEAVFFCNLMQDVHEVSKDKGAICTKLRVPRKRKHGTSAEELARA 226

Db 127 EHYRIMYHASKLISIDEEVYENLMLQVHEHTSDAGLCTRLIKPKVMEGIVAAQDEFYR 186

Qy 227 GWLLNQHLTGAGQEGEGAVLGEYLGQKVAKNIKDVTAQFLDTAVWTKMHE 286

Db 187 GWALNKKELKLQLQTGKGFDVMDYRGNKVAVCKIKNDATAQAFLAESVMTQLRHS 246

Qy 287 NLVRLLGVILHQ--GLYIVMEHVSQGNLVLNFRTRGALVNTAQJQFSLHVACMEYLE 344

Db 247 NLVOLQGVIVEEKGLYVTEYMAKGSLVYDYLRSRGSRVLAGDCLIKESDVCAMEYLE 306

Qy 345 SKKLVIRDLAARNLIVSLEDLVAKVSDFGGLAKAERKGDDSSRLPVIWTAPEALKHCKFTSK 404

Db 307 GNNFVHRLDAARNLIVSLEDNVAKVSDFGGLAKAERKGDDSSRLPVIWTAPEALKHCKFTSK 366

Qy 405 SDWWSFGVILWEVFSYGRAPYKPKMSLKEVSEAVKGYMRPEPPEGCPGPVHLMSSCWEAE 464

Db 367 SDWWSFGILWELMEIYSGRVPYPRFLKDVVPRVERGKYMADPDGCPPAVYEMKNCWHLQ 426

Qy 465 PARRPFKLAEKL 478

Db 427 AATRPFQFLQLEQL 440

RESULT 9

S15094 protein-tyrosine kinase (EC 2.7.1.112) Csk - mouse

N;Alternate names: protein-tyrosine kinase Mpk-2

C;Species: Mus musculus (house mouse)

C;Date: 15-Mar-1995 #sequence_revision 15-Mar-1996 #text_change 18-Feb-2000

C;Accession: I48929; S30498

R;Klages, S.; Adam, D.; Class, K.; Farnol, J.; Bolen, J.B.; Penhallow, R.C. Proc. Natl. Acad. Sci. U.S.A. 91, 2597-2601, 1994

A;Title: Csk: a protein tyrosine kinase related to Csk that defines an enzyme family

A;Reference number: A53469; MUID:9419589; PMID:751815

A;Accession: I48929

A;Molecule type: mRNA

A;Cross-references: EMBL:U05247; NID:9452471; PIDN:AAA18765.1; PID:9452472

R;Giardi, Hebenstreit, P.; Nieto, M.A.; Frain, M.; Mattei, M.G.; Chestier, A.; Wilkin

C;Oncogene 7, 249-2506, 1992

A;Title: An Eph-related receptor protein tyrosine kinase gene segmentally expressed in

R;Lai, C.; Lemke, G.

Neuron 6, 691-704, 1991

A;Title: An extended family of protein-tyrosine kinase genes differentially expressed in

A;Cross-references: EMBL:X58631; NID:957507; PIDN:CAA41484.1; PID:957508

A;Accession: S18500

A;Molecule type: mRNA

A;Cross-accession: PT0183; MUID:9122560; PMID:2025425

A;Molecule type: mRNA

A;Residues: 319-367 <LAI>

A;Experimental source: sciatic nerve

F;82-1717/Domain: SH2 homology <SH2>	F;392,503/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status p
F;193-477/Domain: protein kinase homology <KIN>	Query Match 46.0%; Score 1227.5; DB 2; Length 450;
Best Local Similarity 53.9%; Pred. No. 3e-56;	Matches 165; Conservative 81; Mismatches 153; Indels 25; Gaps 9;
Matches 234; Conservative 81; Mismatches 116; Indels 3; Gaps 2;	Best Local Similarity 38.6%; Pred. No. 3e-32;
Qy 47 WAPGQOCITKCETRPKPGELAFRKGDVVTILEACENKSMWYRKHTSGQEGGLAAGAERALSADPKLSLMPWFH 105	Matches 165; Conservative 81; Mismatches 153; Indels 25; Gaps 9;
Db 8 WPSGTECIARYNFGHTAEQDLPLFCKGDVLTIVAVTFDPNWYKAKNV-GREGITIANYVQ 66	Qy 65 GELARKGDVVTILEACENKSMWYRKHTSGQEGGLAAGAERALSADPKLSLMPWFH 124
Qy 107 EREALSDPKLSLMPWFHKGISQGAVQQLQPPEDGLFLYRESARHHPGDYVLCVSFFGRDV 166	Db 76 GDGLKQKQEKRIVLE--ESEFWRAQSITQGQEGLPHNIVMWNLSLE----PWFF 127
Db 67 KREGVAGTKLISLMPWFHKGITRSGAERLYPEPGLFLYRESTWYPGDVTLCVSCFGKV 126	Qy 125 KRSIGEAVQOLQPPD--GFLVLRBESARHHPGDYVLCV----SFRGDVTHYRVLHD-G 176
Qy 167 THYRVLHRDQHLTIDEAVFFCNLMQDVMEHYSKDKGAICTKLRPKRGHTSAEELARA 226	Db 128 KNLRSKRNAAEYLASCNTHGSSFLIRESETSKGSYSISVRDQNOGETVYHYKFRMDNG 187
Db 127 EHRYTMHASKLISDEEVFFENLQMLQVHEHTDADGLCIRLKRIPKVMGEVTVAQDEFYRS 186	Qy 177 HLTIDEAVFFCNLMQDVMEHYSKDKGAICTKLRPKRGHTSAEELARAQWLNLQHLT 236
Qy 227 GWLNLQHLTGAGQIGEGERGAVLQGEYLGQKQVAKVKNIKDVTAGAFLDETAWMKMQHE 285	Db 188 GYYISPRVTSSLHVELVEYSSSDGICLTRLGKPCR--TQKQPKWWQDWEVPRESLR 244
Db 187 GWALNMKELKLQQTGKGEFGDVMGLDYRGNKVAKCIRKNDATAQAAFLAEASVMTQLRHS 246	Qy 237 LAQIQTGEGERGAVLQGEYLGQ-KVAVKNIK-CDWTAQAFELDETAWMKMOHENLYRLGV 294
Qy 287 NLVRLGVIHQ-G-LYIWEHVSKGKGLWFLRPGRALVNTAQIQLQFSIHWAECEMLE 344	Db 245 DVKEKLAGQFGEWMGFYNGHTKVAQNKLQGMSPLAFLANIMKLNQHPLRVLY 304
Db 247 NLVQLQHVTIVEKSGLVLWVYEMAGSLWYDLSRGSRVSGDQCLIKFSDVLEMEY 305	Qy 355 ARNTLVESEDIAVAKVSDFGLAKA---ERKGIDSSRLPVKMTAPEALKHGKFTSKDSWSE 410
Qy 345 SKKLVHDLAARNITIVSDETLVAKVSDFGLAKAERKGIDSSRLPVKMTAPEALKHGKFTSK 404	Db 365 KANTLVSEACGCKIADFGLARLIEDNEYTAREGAKPEKWKTAPEAINYGT-TIKSDWSE 424
Db 307 GNNFVHFRDLAARNIVYSEDNAVAKVSDFGLTKEASSTQDCKLPPWTAPELREKKFSTK 366	Qy 411 QYLLWEVFSGRAPPKMSIKEVSEAVEGYRMEPEPGCSPGPVHLMSSCWEAEARRPP 470
Qy 405 SDWNSRGVLLWEVFSYGRAPPKMSIKEVSEAVEGYRMEPEPGCSPGPVHLMSSCWEAEARRPP 464	Db 425 GILLLTEIVTGRIPYRPGMTNEVIONLERGYRMPQPDNCPOELYLMQCKEOPPEERT 484
Db 367 SDWNSRGVLLWEVFSYGRIPYRPGMTNEVIONLERGYRMPQPDNCPOELYLMQCKEOPPEERT 426	Qy 471 FRKLAEKL 478
Qy 465 PARRPFKRKAEKL 478	Db 485 FEYMSVYL 492
Db 427 AATRPTFLQLOREQL 440	
RESULT 10	
A39939 protein-tyrosine kinase (EC 2.7.1.112) tkl [similarity] - chicken	
C;Species: Gallus gallus (chicken)	
C;Date: 16-Jun-2000 #sequence_revision 16-Jun-2000 #text_change 16-Jun-2000	
C;Accession: A42126; A39939	
R;Chow, L.M.; Ratcliffe, M.J.; Vellette, A.	
Mol. Cell. Biol. 12, 1226-1233, 1992	
A;Title: tkl is the avian homolog of the mammalian lck tyrosine protein kinase gene.	
A;Reference number: A42126; MUID:92186654; PMID:1545804	
A;Accession: A42126	
A;Molecule type: mRNA	
A;Residues: 1-88 <CCHO>	
A;Cross-references: GB:W85043	
A;Experimental source: thymus, spleen	
A;Note: sequence extracted from NCBI backbone (NCBIN:88831, NCBIRP:88833)	
R;Screbhardt, K.; Mullins, J.I.; Bruck, C.; Ruebsamen-Waigmann, H.	
Proc. Natl. Acad. Sci. U.S.A. 84, 8778-8782, 1987	
A;Title: Additional member of the protein-tyrosine kinase family: the src-and lck-related	
A;Reference number: A39939; MUID:8809/370; PMID:3321053	
A;Accession: A39939	
A;Molecule type: mRNA	
A;Residues: 52-507 <STR>	
A;Cross-references: PID:921712; PIDN:AAA49081_1; PID:921713	
C;Superfamily: protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH3	
C;Keywords: AMP; autophosphorylation; blocked amino end; lipoprotein; myristylation; phc	
C;Key-words: SH3 homology <SH3>	
F;66-114/Domain: SH2 homology <SH2>	
F;125-222/Domain: SH2 homology <SH2>	
F;249-257/Region: protein kinase homology <KIN>	
F;249-257/Region: protein kinase ATP-binding motif	
F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted	
RESULT 11	
148845 protein-tyrosine kinase (EC 2.7.1.112) lck, lymphocyte - mouse	
N;Alternate names: p56; protein-tyrosine kinase tck	
N;Species: Mus musculus (house mouse)	
C;Species: Mus musculus (house mouse)	
C;Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 03-Mar-2000	
C;Accession: 148845; A23639; 157629; I77452	
R;Voronova, A. F.; Sefton, B.M.	
Nature 319, 682-685, 1986	
A;Title: Expression of a new tyrosine protein kinase is stimulated by retrovirus promoter	
A;Reference number: 148845; MUID:86146842; PMID:3081813	
A;Accession: 148845	
A;Status: preliminary; translated from GB/EMBL/DDJB	
A;Molecule type: mRNA	
A;Residues: 1-509 <YOR1>	
A;Cross-references: EMBL:X03533; NID:954813; PIDN:CAA27234_1; PID:954814	
R;Match, J.D.; Peet, R.; Krebs, E.G.; Perlmutter, R.M.	
Cell 43, 393-404, 1985	
A;Title: A lymphocyte specific protein-tyrosine kinase gene is rearranged and overexpressed	
A;Reference number: A23639; MUID:8079521; PMID:2416464	
A;Accession: A23639	
A;Molecule type: mRNA	
A;Residues: 1-282, VP, 285-509 <MAR>	
A;Cross-references: GB:MT2056; NID:9198763	
A;Note: the sequence is revised in GenBank entry MUSLCK, release 116.0, (PIDN:AAB5967	
R;Voronova, A.F.; Adler, H.T.; Sefton, B.M.	
Mol. Cell. Biol. 7, 4407-4413, 1987	
A;Accession: 157629; MUID:88142832; PMID:3501824	
A;Title: Two lck transcripts containing different 5' untranslated regions are present	
A;Reference number: 157629; MUID:88142832; PMID:3501824	
A;Status: preliminary; translated from GB/EMBL/DDJB	
A;Molecule type: DNA	
A;Residues: 1-11 <OR>	
A;Cross-references: GB:MT8098; NID:9198766; PIDN:AAA39421_1; PID:9198767	

Db 78 GDLGFERKGQQLRILE---QSGEWKKAQSLTTGQEGFIPPFNFVAKNSLPEE-----PWF 129
 QY 125 GKTSGQEAQVQOLOPPED---GLFLYRESAHPGDYVLCV---SFGRDWTHYRLHRLG 176
 Db 130 KNLSRKDAKQLLAPGNTGGSFLIRESESTAGSFSLSVRDFDQNQGEVVKHYKIRNLNG 189
 QY 177 HLTIDEAVFCNLMDMVEHYSKOGAIC"KLVRPKRKHGKTSAAEELARRAGWLNLQHIT 236
 Db 190 GFYIISPRITPGLHLVRLVHYNASDGLCITRLSRPCQ---TOKOPKPWNEDEWEVPRETR 246
 QY 237 LGAQIGEGERGAVIQLQGEYQGO-KVAVKNK-CDVTAQAFDPAVMTKQHENIVRLIGV 294
 Db 247 LVERIGAGCQFGEVNGVYVNGHTKAVSKQGKSHSPDPALEANLMKQHQRLVRLIYAV 306
 QY 295 ILHQGLYTMHEVSKGNLNUFLRTRGRALVNTAOLLOFLSILHVARGMEVYESKKLVHROIA 354
 Db 307 VTQEPPIVITTEYIMENGSLVDFLKTPSGIKLTINKLDMQAQIAEGMAFEERNYIHDRL 366
 QY 355 ARNLTLSEDLVAKVSKDFGLAKA---ERGLDSSRLPVWTAPEALKHGKFTSKSDWNSF 410
 Db 367 AANILVSDALSLCKLADFGIARLICDNEYTAREGAKFPTKTAPEAINYGTFTKSDWNSF 426
 Qy 411 GVLILMEVFSYGRALYQPKMSLKEVSEANEGYMRPPEGGPGPVAVLMSSCWEAPRAPP 470
 Db 427 GILLTTEIVFHGRIPYPGMNPEVTONLEGYRMYVRPDNPEEELYQMLRUCWKERPEDRPT 486
 QY 471 FRKLAELK 478
 Db 487 FDYLVRSVL 494

RESULT 13

S5313 protein-tyrosine kinase (EC 2.7.1.112) src - Rous sarcoma virus

C;Species: Rous sarcoma virus
 C;Date: 08-May-1995 #sequence_revision 21-Jul-1995 #text_change 04-Mar-2000
 C;Accession: S52313
 R;ratsoyan, A.; Yatsula, B.; Shtrutman, M.; Moihova, E.; Kaverina, I.; Musatkina, E.; Les submitted to the EMBL Data Library, January 1995
 A;Description: Two new isoforms of v-src oncogene isolated from low and high metastatic A;Accession: S52313
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-545 <TAT>
 A;Cross-references: EMBL:X84074; NID:9663083; PIDN:CAA58891.1; PID:9663084
 C;Superfamily: protein-tyrosine kinase src; protein kinase homology; SH3 homology; SH3 R
 C;Keywords: Rtp; autophosphorylation; blocked amino end; lipoprotein; myristylation; pho
 F;108-157/Domain: SH3 homology <SH3>
 F;168-265/Domain: SH2 homology <SH2>
 F;285-543/Domain: protein kinase homology <KIN>
 F;293-301/Region: protein kinase Atp-binding motif
 F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
 F;315/Active site: Lys #status predicted
 F;436/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted
 Query Match 27.6% Score 736; DB 2; Length 555;
 Best Local Similarity 35.6%; Pred. No. 7.3e-31; Matches 82; Mismatches 181; Indels 76; Gaps 16;
 QY 14 HGCDSAEELP-----VSPEFLRAWH-----PWSARMTRRHPG----- 51
 Db 26 HGGFPASOPNPKTAPLTAAPRSSR--RPPASQHRAADTHPPRSF---GTVANEPEKF 81
 QY 52 -----QCTTKCEITRPRKG-----ELAFRKGDVVTILEACENKSNWR 88
 Db 82 GDFWISDVTISPSQARTLPGGTVFVALYDYESWIEITDLSFKGERQIVNTEG 140
 QY 89 VKHHTSGQGGLAAGALRREALSDAPKSLIMMWFHKGKSGQRAVQKQOPPED---GLFLY 146
 Db 141 AHSVTGKTYGIPSNYVAPSDSIQE-----EWYFGKTRRSGLLNPENPGRFLV 194
 QY 147 RESARHPGDQWICVS---FGDQVHIVVFLHD-GHITIDEAVFCNLMDMVEHYSRKA 200

RESULT 14

TVCHS protein-tyrosine kinase (EC 2.7.1.112) src - chicken

N;Alternate names: kinase-related transforming protein src
 C;Species: Gallus gallus (chicken)
 C;Accession: A00630; MUID:8315564; PMID:629580
 C;Accession: A00630; 150217; A41256; C35650; A32432
 R;Takeya, T.; Hanafusa, H.
 Cell 32, 881-890, 1983
 A;Title: Structure and sequence of the cellular gene homologous to the RSV src gene a
 A;Reference number: A00630
 A;Accession: A00630
 A;Molecule type: DNA
 A;Residues: 1-500, 'R' 502-533 <TAK>
 A;Cross References: GB:J00844; NID:9212700
 R;Takeya, T.; Hanafusa, H.
 Cell 34, 319, 1983
 A;Reference number: A90838
 A;Contents: annotation; erratum; correct translation of residue 526
 R;Takeya, T.; Hanafusa, H.
 J. Virol. 44, 12-18, 1982
 A;Title: DNA sequence of the viral and cellular src gene of chickens: II comparison o
 A;Reference number: 150217; MUID:83059861; PMID:629480
 A;Accession: 150217
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-7 <TA>
 A;Cross-references: GB:J00808; NID:g211690; PIDN:AA44873.1; PID:9211691
 A;Note: the authors translated the codons AAC and CAG for residues 301 and 526 as Thr
 R;boraI, T.; Levy, J.B.; Kang, L.; Brugge, J.S.; Wang, L.H.
 Mol. Cell. Biol. 11, 4165-176, 1991
 A;Reference number: A1256; MUID:91304409; PMID:1712905
 A;Accession: A41256
 A;Molecule type: mRNA
 A;Residues: 484-533 <DOR1>
 A;Cross-references: GB:S43579; NID:91679954; PIDN:AB19353.1; PID:9233061
 A;Note: the authors translated the codon CAG for residue 527 as Glu
 R;Durai, T.; Wang, L.H.
 Mol. Cell. Biol. 10, 4068-4079, 1990
 A;Reference number: A35650; MUID:90318371; PMID:211517
 A;Accession: C35650
 A;Molecule type: mRNA
 A;Residues: 1-182, 'DPCIPLPSCIC' <DOR2>
 A;Cross-references: GB:W5790; NID:9312703; PIDN:AA449078.1; PID:9212706
 A;Note: alternatively spliced mRNA exclusively replaces the long-form in skeletal muscle
 A;Note: this ORF appears not to be translated
 R;Shenoy, S.; Choi, J.K.; Bagrodia, S.; Copeland, T.D.; Maller, J.L.; Shalloway, D.

Cell 57, 763-774, 1989
 A;Title: Purified maturation promoting factor phosphorylates pp60(c-src) at the sites phe-
 A;Reference number: A32432; MUID:89249341; PMID:2470512
 A;Accession: A32432
 A;Molecule type: protein
 A;Residues: 2-88 <SHE>
 A;Note: 34-Thr, 46-Thr, and 72-Ser are phosphorylated during mitosis
 C;Genetics:
 A;Gene: src
 C;Superfamily: protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH3 homology
 C;Keywords: alternative splicing; ATP; autophosphorylation; blocked amino end; lipoprotein
 F;18-137/Domain: SH2 homology <SH2>
 F;18-245/Domain: SH2 homology <SH2>
 F;205-523/Domain: protein kinase homology <KIN>
 F;273-281/Region: protein kinase homology <KIN>
 F;273/281/Region: protein kinase homology <KIN>
 F;273/281/Region: protein kinase homology <KIN>
 F;12,48/Binding site: phosphate (Ser) (covalent) (by protein kinase A) #status predicted
 F;12,48/Binding site: phosphate (Ser) (covalent) (by protein kinase A) #status predicted
 F;31,46/Binding site: phosphate (Thr) (covalent) #status experimental
 F;72/2/Binding site: phosphate (Ser) (covalent) #status predicted
 F;72/2/Binding site: phosphate (Ser) (covalent) #status experimental
 F;416,521/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted
 Query Match 27.5%; Score 735; DB 1; Length 533;
 Best Local Similarity 37.9%; Pred. No. 8e-31;
 Matches 173; Conservative 79; Mismatches 31; Indels 42; Gaps 11;
 QY 66 ELAFRKGDVVTILEACENKSWYRKHTSGOGLLAAGALREREALSDAPKLSLMPWFHG 125
 Db 99 DLSFKKERQLOQIVNTEG-NWMLAISLTGQTYIPSINYVAPSDIQAE-----EWFG 151
 QY 126 KISGQAVQQLQPPED--GLFLVRESRARHGDYVLCVSG---FGRDVHRYVLRD-GH 177
 Db 152 KITRRESERLLNPNENPRGFLVRESEETKGAYCLSVSDFDNAKGLNVKHKIRKLDGG 211
 QY 178 LTIDEAVFFCNLMDVHEYHKDKGAICTKL--VRRRKHGKSAEELARAGWLNLQHL 235
 Db 212 FYITSRTOFQSSILQQLQVAYSKSHADGLCHRLTNVCPKSPQPOQG---LAKDAWEIPRESL 267
 QY 236 TLGAQIGEGERGAVLOGEYLG-QKAVAKNKR-CDYTAQAFDETAVMTKQHENLYVRLLG 293
 Db 268 RLEVKGQGQGERGEWNGTWTGTTWRAIKTLPKGNSPEAQFQEAQYMKHLRKEHVQLYA 327
 QY 294 VILHQGLYTMEHVSQGNLVNLFLTRGRALVNTAQOLQFLSHVAEGMELESKKLVHDL 353
 Db 328 WVSERPIVYIYEIMSKSLDFLKGEMGKYLRLPQVDMQAQISGMAVYERMVYHDL 387
 QY 354 AARNLIVSEDIVAKVSDFGLAKA---ERKGLDSRSLPVWVTPAPELLKHKFTSKDWWS 409
 Db 388 RAANLIVGLENVCKYADFLGLARLIEDNEYTARQGAKFPKWTAPEALEYGRTFSDWS 447
 QY 410 FGVLQMEVFSYGRAYQPKMSLKEVSEAVKQYRMPPEGCPGPVHMLSSCWEAEPARRP 469
 Db 448 FGILQTLTETLKGVRVYQPMNREVIDQVEMQYRMCPPECPPESELIDIMOCWKRKEERP 507
 QY 470 PFRKLAELKARELRSAGAPASVSGODADGSTSPRSQ 505
 Db 508 TFEYIQLAFL-----EDYFISTERPQO 528
 RESULT 15
 TVFVG0
 protein-tyrosine kinase (EC 2.7.1.112) src - Rous sarcoma virus
 C;Species: Rous sarcoma virus
 C;Accession: 22-May-1981 #sequence_revision 17-Dec-1982 #text_change 24-Sep-1999
 C;Date: 22-May-1981
 C;Accession: A38017; A00631; S0226; A38018
 R;Czerniolsky, A.P.; Levinson, A.D.; Varmus, H.E.; Bishop, J.M.; Tischer, E.; Goodman, Nature 301, 736-738, 1983
 A;Title: Corrections to the nucleotide sequence of the src gene of Rous sarcoma virus.
 A;Reference number: A38017; MUID:83141780; PMID:6298633
 A;Accession: A38017
 A;Molecule type: DNA
 A;Residues: 1-526 <CZER>
 A;Cross-references: GB:L29199; GB:J02018; GB:J02026; GB:J02352; GB:K01194; GB:K01195;
 A;Experimental source: strain Schmidt-Ruppin
 R;Takeya, T.; Hanafusa, H.
 Cell 32, 881-890, 1983
 A;Title: Structure and sequence of the cellular gene homologous to the RSV src gene a
 A;Reference number: A00630; MUID:8315564; PMID:6299580
 A;Accession: A00631
 A;Molecule type: DNA
 A;Residues: 1-62, 'D', 64-95, 'T', 97-123, 'V', 125-300, 'N', 302-526 <PAK>
 A;Experimental source: strain Schmidt-Ruppin
 R;Barnier, J.V.; Doreelee, P.; Marx, M.; Calothy, G.
 Nucleic Acids Res. 17, 1252, 1989
 A;Title: Nucleotide sequence of the src gene of the Schmidt-Ruppin strain of Rous Sarcoma virus
 A;Reference number: S02726; MUID:89160256; PMID:2537953
 A;Accession: S02726
 A;Molecule type: DNA
 A;Residues: 1-9, 'G', 11-62, 'D', 64-123, 'V', 125-319, 'K', 321-495, 'S', 497-526 <BAR>
 A;Cross-references: EMBL:X13145; MBD:95080; PIDN:CAR32012.1; PID:961909
 R;Takeya, T.; Feldman, R.A.; Hanafusa, H.
 J. Virol. 44, 1-11, 1982
 A;Title: DNA sequence of the viral and cellular src gene of chickens: I. complete nucleotide sequence
 A;Reference number: A38018; MUID:83059858; PMID:6292477
 A;Accession: A38018
 A;Molecule type: DNA
 A;Residues: 1-15, 'C', 17-94, 'R', 97-116, 'D', 118-337, 'T', 339-526 <TA2>
 A;Cross-references: GB:K02028; MBD:92010187; PIDN:AAA42565.1; PID:92010189
 A;Experimental source: strain rASY141
 R;Neill, J.C.; Glysaeel, J.; Vogt, P.K.; Smart, J.E.
 Nature 291, 675-677, 1981
 A;Title: Homologous tyrosine phosphorylation sites in transformation-specific gene pRb
 A;Reference number: A38019; MUID:8220979; PMID:62464320
 A;Comments: The sequence from the Schmidt-Ruppin strain is shown.
 C;Genetics:
 A;Gene: src
 C;Superfamily: protein-tyrosine kinase homology <SH3>
 F;14-24/Domain: SH2 homology <SH3>
 F;265-523/Domain: protein kinase homology <KIN>
 F;273-281/Region: protein kinase homology <KIN>
 F;273/281/Region: protein kinase homology <KIN>
 F;273/281/Region: protein kinase homology <KIN>
 F;295/Active site: Lys #status predicted
 F;416/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted
 Query Match 27.5%; Score 734.5; DB 1; Length 526;
 Best Local Similarity 39.2%; Pred. No. 8.4e-31;
 Matches 168; Conservative 78; Mismatches 156; Indels 27; Gaps 10;
 QY 66 ELAFRKGDVVTILEACENKSWYRKHTSGOGLLAAGALREREALSDAPKLSLMPWFHG 125
 Db 99 DLSFKKERQLOQIVNTEG-NWMLAISLTGQTYIPSINYVAPSDIQAE-----EWFG 151
 QY 126 KISGQAVQQLQPPED--GLFLVRESRARHGDYVLCVSG---FGRDVHRYVLRD-GH 177
 Db 152 KITRRESERLLNPNENPRGFLVRESEETKGAYCLSVSDFDNAKGLNVKHKIRKLDGG 211
 QY 178 LTIDEAVFFCNLMDVHEYHKDKGAICTKL--VRRRKHGKSAEELARAGWLNLQHL 235
 Db 212 FYITSRTOFQSSILQQLQVAYSKSHADGLCHRLTNVCPKSPQPOQG---LAKDAWEIPRESL 267
 QY 236 TLGAQIGEGERGAVLOGEYLG-QKAVAKNKR-CDYTAQAFDETAVMTKQHENLYVRLLG 293
 Db 268 RLEVKGQGQGERGEWNGTWTGTTWRAIKTLPKGNSPEAQFQEAQYMKHLRKEHVQLYA 327
 QY 294 VILHQGLYTMEHVSQGNLVNLFLTRGRALVNTAQOLQFLSHVAEGMELESKKLVHDL 353
 Db 328 WVSERPIVYIYEIMSKSLDFLKGEMGKYLRLPQVDMQAQISGMAVYERMVYHDL 387
 QY 354 AARNLIVSEDIVAKVSDFGLAKA---ERKGLDSRSLPVWVTPAPELLKHKFTSKDWWS 409
 Db 388 RAANLIVGLENVCKYADFLGLARLIEDNEYTARQGAKFPKWTAPEALEYGRTFSDWS 447

QY 410 FGVLWEVSYGRAPKMSLKEYSEAVRGYRAMEPPECPGPVPHVLMSCWEAREP 469
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | |
Db 448 FGILTELTRKGVPYPMGNGEVLDYRMPCCPESLHDLMQCRDPEERP 507

QY 470 PFRKLAEKL 478
| | | : |
Db 508 TFEYLOAQL 516

Search completed: July 29, 2003, 09:53:03
Job time : 25 secs

OM protein - protein search, using sw model

Run on: July 29, 2003, 09:51:02 ; search time 27 seconds
(without alignments)
2230.045 million cell updates/sec

Title: US-09-977-261-2

Perfect score: 261

Sequence: 1 MAGRGSLLSVWRAFHGCDSAE....., PAVSGQDADGSTSPRSQEP 507

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 451899 seqs, 118759770 residues

Total number of hits satisfying chosen parameters: 451899

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Published Applications_AA:*

1: /cgtr2_6/ptodata/2/pubpea/US07_PUBCOMB.pep:*

2: /cgtr2_6/ptodata/2/pubpea/PCT_NEW_PUB.pep:*

3: /cgtr2_6/ptodata/2/pubpea/US05_NEW_PUB.pep:*

4: /cgtr2_6/ptodata/2/pubpea/US06_PUBCOMB.pep:*

5: /cgtr2_6/ptodata/2/pubpea/US07_NEW_PUB.pep:*

6: /cgtr2_6/ptodata/2/pubpea/PCMUS_PUBCOMB.pep:*

7: /cgtr2_6/ptodata/2/pubpea/US08_NEW_PUB.pep:*

8: /cgtr2_6/ptodata/2/pubpea/US08_PUBCOMB.pep:*

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10: /cgtr2_6/ptodata/2/pubpea/US09B_PUBCOMB.pep:*

11: /cgtr2_6/ptodata/2/pubpea/US09C_PUBCOMB.pep:*

12: /cgtr2_6/ptodata/2/pubpea/US09_NEW_PUB.pep:*

13: /cgtr2_6/ptodata/2/pubpea/US10A_PUBCOMB.pep:*

14: /cgtr2_6/ptodata/2/pubpea/US10B_PUBCOMB.pep:*

15: /cgtr2_6/ptodata/2/pubpea/US10C_PUBCOMB.pep:*

16: /cgtr2_6/ptodata/2/pubpea/US10_NEW_PUB.pep:*

17: /cgtr2_6/ptodata/2/pubpea/US10_NEW_PUB.pep:*

18: /cgtr2_6/ptodata/2/pubpea/US10_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2671	100.0	507	9	US-09-977-269-2
2	2671	100.0	507	10	US-09-977-260-2
3	2671	100.0	507	11	US-09-977-261-2
4	1245.5	46.6	450	9	US-09-977-269-7
5	1245.5	46.6	450	10	US-09-977-260-7
6	1245.5	46.6	450	11	US-09-977-261-7
7	1245.5	46.6	450	15	US-10-059-585-42
8	1245.5	46.6	450	15	US-10-177-293-88
9	1245.5	46.6	450	16	US-10-298-377A-2
10	916	34.3	357	11	US-09-929-266-9
11	768	28.8	258	10	US-09-840-704-3
12	742.5	27.8	509	9	US-09-977-269-18
13	742.5	27.8	509	10	US-09-977-260-18
14	742.5	27.8	509	11	US-09-977-261-17
15	727	27.2	536	9	US-09-977-269-13

RESULT 1
US-09-977-269-2

; Sequence 2, Application US/09977269

; Patent No. US20030082037A1

; GENERAL INFORMATION:

; APPLICANT: ULLRICH, AXEL

; APPLICANT: GISZKZY, MIKAEL

; APPLICANT: SURSIS, IRMINGARD

; TITLE OF INVENTION: NOVEL MEGAKARYOCYTIC PROTEIN TYROSINE KINASES

; FILE REFERENCE: 03860/1/250

; CURRENT APPLICATION NUMBER: US/09/977, 269

; PRIORITY APPLICATION NUMBER: 08/232, 545

; PRIORITY FILING DATE: 1994-04-22

; NUMBER OF SEQ ID NOS: 24

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 2 LENGTH: 507

; TYPE: PRT

; ORGANISM: Unknown Organism

; FEATURE:

; OTHER INFORMATION: Description of Unknown organism: Megakaryocyte

; OTHER INFORMATION: kinase 1

; OTHER INFORMATION: kinase 1

Query Match 100.0%; Score 2671; DB 9; Length 507;

Best Local Similarity 100.0%; Pred. No. 6.7e-209;

Matches 507; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAGRGSLLSVWRAFHGCDSAEELPLRVSPLRFLRWAHPPVSARMPTWRAPGTCITKCENT 60

Db 1 MAGRGSLLSVWRAFHGCDSAEELPLRVSPLRFLRWAHPPVSARMPTWRAPGTCITKCENT 60

Qy 61 RPKPEBLAFRGDVTILEACENKSKWYRVKHTSTSQEGLAAAGARERELASAPPKLSM 120

Db 61 RPKPEBLAFRGDVTILEACENKSKWYRVKHTSTSQEGLAAAGARERELASAPPKLSM 120

Qy 121 PWFHIGKISQGAEVQQLQPPEPDGLFVYRESARHPGDYLVCVSGFRDVHVLHRDHGHT 180

RESULT 4
US-09-977-269-7
; Sequence 7, Application US/09977269
; GENERAL INFORMATION:
; APPLICANT: GISZIKY, MIKHAIL
; APPLICANT: SURES, IRMINGARD
; APPLICANT: ULLRICH, AXEL
; APPLICANT: ULLRICH, AXEL
; APPLICANT: GISZIKY, MIKHAIL
; APPLICANT: SURES, IRMINGARD
; APPLICANT: ULLRICH, AXEL
; TITLE OF INVENTION: NOVEL MEGAKARYOCYTIC PROTEIN TYROSINE KINASES
; FILE REFERENCE: 038602/1260
; CURRENT APPLICATION NUMBER: US/09/977,269
; CURRENT FILING DATE: 2001-10-16
; PRIORITY APPLICATION NUMBER: 08/232,545
; PRIORITY FILING DATE: 1994-04-22
; NUMBER OF SEQ ID NOS: 24
; LENGTH: 450
; SEQ ID NO: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-977-269-7
Query Match 45.6%; Score 1245.5; DB 9; length 450;
Best Local Similarity 54.1%; Pred. No. 4.4e-93;
Matches 235; Conservative 81; Mismatches 115; Indels 3; Gaps 2;
Query 47 WAPGTQCTKCEHTPKPGCLAFRKGDVVTLAECEENKSMYRVKHTSQEGLLAAGAIR 106
Db 8 WPSGFECIARYNFGHTAEQDLPFECGVDLIVAVKDPWYKAKNV-GREGIIPANYQ 66
Query 107 EREALSADPKLUSLMPWFHGKTSQGAVQQLQPPEGLFLVRESARHPGQYVLCVSGRDY 166
Db 67 KREGVKAGTKLUSLMPWFHGKTRDQAERLYPPETGFLFVRESTNYPGTYLCVSCDGKV 126
Query 167 THYRVLHRDGHLTIDEAVFCNLMMVHEYSKDKGAICTKLVRKRKGTSKABELARA 226
Db 127 EHRYIMHASKLISIDEEVFENLMLQVHEHTSDAGLCIRLRIKPMEGTVAQDEFYRS 186
Query 227 GWLNLQHUTLGAQIGEGERGAVIQLGEYIGQVAKVKNICDVTAQAFDUTAVMKMRE 286
Db 187 GWALKMKELKLQQTIGKGEFGDVMGQDGRNPKVAKCIRKNDATAQAFLEAASWMTQLRHS 246
Query 287 NLVRILGVILHQ-G-GLYIYEHVSGNQUNFLRGRALVNTAQLQSLHVAEGMEYLE 344
Db 247 NLVQDGLVITVEKEGLYIVTEYMAKGSVLDYLSRGRGSVLYGDCDLILFSLDUDCEAME 306
Query 345 SKKLVHRDIAARNLIVSEDIWAKSDFGLAKAERKGLDSSRLPKWTADEALKHGKFTSK 404
Db 307 GNNFVHRDIAARNLIVSEDNAVKSDFGLKKEASSTQDCKLPKWTABALRKFKSK 366
Query 405 SDWMSFGVILWEVSYGRAPYKMSLKEVEAVERGYRMEPPEGGCPGPVHLMSCWEA 464
Db 367 SDWMSFGVILWEVSYGRAPYKMSLKEVEAVERGYRMEPPEGGCPGPVHLMSCWEA 426
Query 481 ELRSAGAPSVSGQDAGTSRSPQEP 507
Db 481 ELRSAGAPSVSGQDAGTSRSPQEP 507
RESULT 5
US-09-977-260-7
; Sequence 7, Application US/09977260
; Publication No. US20020192790A1
; GENERAL INFORMATION:
; APPLICANT: GISZIKY, MIKHAIL
; APPLICANT: SURES, IRMINGARD
; APPLICANT: ULLRICH, AXEL
; APPLICANT: GISZIKY, MIKHAIL
; APPLICANT: SURES, IRMINGARD
; APPLICANT: ULLRICH, AXEL
; TITLE OF INVENTION: NOVEL MEGAKARYOCYTIC PROTEIN TYROSINE KINASES
; FILE REFERENCE: 038602/1260
; CURRENT APPLICATION NUMBER: US/09/977,260
; CURRENT FILING DATE: 2001-10-16
; PRIORITY APPLICATION NUMBER: 08/232,545
; PRIORITY FILING DATE: 1994-04-22
; NUMBER OF SEQ ID NOS: 24
; LENGTH: 450
; SEQ ID NO: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-977-260-7
Query Match 46.6%; Score 1245.5; DB 10; length 450;
Best Local Similarity 54.1%; Pred. No. 4.4e-93;
Matches 235; Conservative 81; Mismatches 115; Indels 3; Gaps 2;
Query 47 WAPGTQCTKCEHTPKPGCLAFRKGDVVTLAECEENKSMYRVKHTSQEGLLAAGAIR 106
Db 8 WPSGFECIARYNFGHTAEQDLPFECGVDLIVAVKDPWYKAKNV-GREGIIPANYQ 66
Query 107 EREALSADPKLUSLMPWFHGKTSQGAVQQLQPPEGLFLVRESARHPGQYVLCVSGRDY 166
Db 67 KREGVKAGTKLUSLMPWFHGKTRDQAERLYPPETGFLFVRESTNYPGTYLCVSCDGKV 126
Query 167 THYRVLHRDGHLTIDEAVFCNLMMVHEYSKDKGAICTKLVRKRKGTSKABELARA 226
Db 127 EHRYIMHASKLISIDEEVFENLMLQVHEHTSDAGLCIRLRIKPMEGTVAQDEFYRS 186
Query 227 GWLNLQHUTLGAQIGEGERGAVIQLGEYIGQVAKVKNICDVTAQAFDUTAVMKMRE 286
Db 187 GWALKMKELKLQQTIGKGEFGDVMGQDGRNPKVAKCIRKNDATAQAFLEAASWMTQLRHS 246
Query 287 NLVRILGVILHQ-G-GLYIYEHVSGNQUNFLRGRALVNTAQLQSLHVAEGMEYLE 344
Db 247 NLVQDGLVITVEKEGLYIVTEYMAKGSVLDYLSRGRGSVLYGDCDLILFSLDUDCEAME 306
Query 345 SKKLVHRDIAARNLIVSEDIWAKSDFGLAKAERKGLDSSRLPKWTADEALKHGKFTSK 404
Db 307 GNNFVHRDIAARNLIVSEDNAVKSDFGLKKEASSTQDCKLPKWTABALRKFKSK 366
Query 405 SDWMSFGVILWEVSYGRAPYKMSLKEVEAVERGYRMEPPEGGCPGPVHLMSCWEA 464
Db 367 SDWMSFGVILWEVSYGRAPYKMSLKEVEAVERGYRMEPPEGGCPGPVHLMSCWEA 426
Query 481 ELRSAGAPSVSGQDAGTSRSPQEP 507
Db 481 ELRSAGAPSVSGQDAGTSRSPQEP 507
RESULT 6
US-09-977-261-7
; Sequence 7, Application US/09977261
; Publication No. US20030054527A1
; GENERAL INFORMATION:
; APPLICANT: ULLRICH, AXEL
; APPLICANT: GISZIKY, MIKHAIL
; APPLICANT: SURES, IRMINGARD
; APPLICANT: ULLRICH, AXEL
; APPLICANT: GISZIKY, MIKHAIL
; APPLICANT: SURES, IRMINGARD
; APPLICANT: ULLRICH, AXEL
; TITLE OF INVENTION: NOVEL MEGAKARYOCYTIC PROTEIN TYROSINE KINASES
; FILE REFERENCE: 038602/1259
; CURRENT APPLICATION NUMBER: US/09/977,261
; CURRENT FILING DATE: 2001-10-16
; PRIORITY APPLICATION NUMBER: 08/232,545
; PRIORITY FILING DATE: 1994-04-22

NUMBER OF SEQ ID NOS: 24
 SOFTWARE: PatentIn ver. 2.1
 SEQ ID NO: 7
 LENGTH: 450
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-977-261-7

Query Match 46.6%; Score 1245.5; DB 11; Length 450;
 Best Local Similarity 54.1%; Pred. No. 4.4e-93;
 Matches 235; Conservative 81; Mismatches 115; Indels 3; Gaps 2;

QY 47 WAPGTCITKCHTRPKGELAFRKGVVTLAEACENKSWRYKHTSQEGILAGAIR 106
 8 WPSGTECIAKYNFHGTAEQDLPCKGDVLTIVATVKDPNWYAKNKV-GREGIIPANYQ 66

QY 107 EREALSADPKLSIMPWFHGKISQEAQVQLOQPPEDGLFLVRESARHGPDYVLCVSFRDV 166
 67 KREGVKGKTSLIMPWFHGKTRREQEALRLLPPETGLFLVRESNTNPGDYVLCVSFRDV 126

QY 167 HYRVLHRDGHLTIDEAVFFCNLMDMVHYSKDKGAICTKLYRKPKRGTKSAEELARA 226
 127 EHRYIMHASKLUSIDEEVYFENIMLQMVLYHPTSDADGLCIRLKPMEGTVAQDEFYRS 186

QY 227 GWLNLOHLTGAQIGEFGAVLQGEVLQGKQAVKNIKCDTAQAFDETAMTKMHE 286
 187 GWALNMKELKLQITGKGEFGDVMGLGDYRGNKAVKCTKINDATAQAFLAESTMQLRHS 246

QY 287 NIVRLIGVILHQ-GLYTIVMHEVSKGNIVNLFTRGRALVNTAQQLQSLHVAEGMYLE 344
 247 NIVQOLIGVIVEKGGLYVTEMAKSLVYDYLRSGRVSLGQCLKSLDVCEAMEYLE 306

QY 345 SKRLVHDLAARNILVSEDLVAKVSDRGLAKAERKGKGLDSSRLPVKWTAPEALKHGKFTSK 404
 307 GNNFVHRDLAARNVLVSEDNVAKVSDFGLTKEASSTQDTGKLPVKWTAPEALKFSTK 366

QY 405 SDWWSFGVLLMEVFSGRVPPYPRIPKDVYPRVEKGYKMDADPGCPPAVYEVNKNCHLD 464
 367 SDWWSFGVLLMEVFSGRVPPYPRIPKDVYPRVEKGYKMDADPGCPPAVYEVNKNCHLD 426

QY 465 PARRPPFKLAEL 478
 Db 427 AAMRPSFLQLRQL 440

RESULT 7

US-10-059-585-42

; Sequence 42, Application US/10059585
 ; Publication No. US20030082776A1

GENERAL INFORMATION:

APPLICANT: Ota, Toshio
 APPLICANT: Isogai, Takao
 APPLICANT: Nishikawa, Tetsuo
 APPLICANT: Hayashi, Koji
 APPLICANT: Otsuka, Kaoru
 APPLICANT: Yamamoto, Jun-ichi
 APPLICANT: Ishii, Shizuko
 APPLICANT: Sugiyama, Tomoyasu
 APPLICANT: Wakamatsu, Ai
 APPLICANT: Nagai, Keiichi
 APPLICANT: Otsuki, Tetsuji
 APPLICANT: Funahashi, Shin-ichi
 APPLICANT: Senoo, Chiaki
 APPLICANT: Nezu, Jun-ichi

TITLE OF INVENTION: NOVEL GENES ENCODING PROTEIN
 FILE REFERENCE: 05501-098001

CURRENT FILING DATE: 2002-01-29
 PRIOR APPLICATION NUMBER: PCT/JP00/05060
 PRIOR FILING DATE: 2000-07-28
 PRIOR APPLICATION NUMBER: US 60/183,322
 PRIOR FILING DATE: 2000-02-17

Query Match 46.6%; Score 1245.5; DB 15; Length 450;
 Best Local Similarity 54.1%; Pred. No. 4.4e-93;
 Matches 235; Conservative 81; Mismatches 115; Indels 3; Gaps 2;

QY 47 WAPGTCITKCHTRPKGELAFRKGVVTLAEACENKSWRYKHTSQEGILAGAIR 106
 8 WPSGTECIAKYNFHGTAEQDLPCKGDVLTIVATVKDPNWYAKNKV-GREGIIPANYQ 66

QY 107 EREALSADPKLSIMPWFHGKISQEAQVQLOQPPEDGLFLVRESARHGPDYVLCVSFRDV 166
 67 KREGVKGKTSLIMPWFHGKTRREQEALRLLPPETGLFLVRESNTNPGDYVLCVSFRDV 126

QY 167 HYRVLHRDGHLTIDEAVFFCNLMDMVHYSKDKGAICTKLYRKPKRGTKSAEELARA 226
 127 EHRYIMHASKLUSIDEEVYFENIMLQMVLYHPTSDADGLCIRLKPMEGTVAQDEFYRS 186

QY 227 GWLNLOHLTGAQIGEFGAVLQGEVLQGKQAVKNIKCDTAQAFDETAMTKMHE 286
 187 GWALNMKELKLQITGKGEFGDVMGLGDYRGNKAVKCTKINDATAQAFLAESTMQLRHS 246

QY 287 NIVRLIGVILHQ-GLYTIVMHEVSKGNIVNLFTRGRALVNTAQQLQSLHVAEGMYLE 344
 247 NIVQOLIGVIVEKGGLYVTEMAKSLVYDYLRSGRVSLGQCLKSLDVCEAMEYLE 306

QY 345 SKRLVHDLAARNILVSEDLVAKVSDRGLAKAERKGKGLDSSRLPVKWTAPEALKHGKFTSK 404
 307 GNNFVHRDLAARNVLVSEDNVAKVSDFGLTKEASSTQDTGKLPVKWTAPEALKFSTK 366

QY 345 SKRLVHDLAARNILVSEDLVAKVSDRGLAKAERKGKGLDSSRLPVKWTAPEALKHGKFTSK 404
 307 GNNFVHRDLAARNVLVSEDNVAKVSDFGLTKEASSTQDTGKLPVKWTAPEALKFSTK 366

QY 405 SDWWSFGVLLMEVFSGRVPPYPRIPKDVYPRVEKGYKMDADPGCPPAVYEVNKNCHLD 464
 367 SDWWSFGVLLMEVFSGRVPPYPRIPKDVYPRVEKGYKMDADPGCPPAVYEVNKNCHLD 426

QY 465 PARRPPFKLAEL 478
 Db 427 AAMRPSFLQLRQL 440

RESULT 8

US-10-177-293-88

; Sequence 88, Application US/10177-293
 ; Publication No. US2003124128A1

GENERAL INFORMATION:

APPLICANT: Lillie, James
 APPLICANT: Glatt, Karen
 APPLICANT: Zhao, Xumei
 APPLICANT: Gannavarapu, Manjula
 APPLICANT: Kamatkar, Shubhangi
 APPLICANT: Mertens, Maureen
 APPLICANT: Myer, Vic
 APPLICANT: Wang, Youzhen
 APPLICANT: Xu, Yongyao
 APPLICANT: Hoersch, Sebastian
 APPLICANT: Monahan, John
 APPLICANT: Meyers, Rachel E.
 APPLICANT: Bast, Jr., Robert C.
 APPLICANT: Hortobagyi, Gabriel N.
 APPLICANT: Puszai, Lajos

PRIOR APPLICATION NUMBER: US 60/159,590
 PRIOR FILING DATE: 1999-10-18
 PRIOR APPLICATION NUMBER: JP 2000-118776
 PRIOR FILING DATE: 2000-01-11
 PRIOR APPLICATION NUMBER: JP 2000-183767
 PRIOR FILING DATE: 2000-05-02
 PRIOR APPLICATION NUMBER: JP 11-248036
 PRIORITY FILING DATE: 1999-07-29
 NUMBER OF SEQ ID NOS: 64
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 42
 LENGTH: 450
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-059-585-42

Query Match 46.6%; Score 1245.5; DB 15; Length 450;
 Best Local Similarity 54.1%; Pred. No. 4.4e-93;
 Matches 235; Conservative 81; Mismatches 115; Indels 3; Gaps 2;

QY 47 WAPGTCITKCHTRPKGELAFRKGVVTLAEACENKSWRYKHTSQEGILAGAIR 106
 8 WPSGTECIAKYNFHGTAEQDLPCKGDVLTIVATVKDPNWYAKNKV-GREGIIPANYQ 66

QY 107 EREALSADPKLSIMPWFHGKISQEAQVQLOQPPEDGLFLVRESARHGPDYVLCVSFRDV 166
 67 KREGVKGKTSLIMPWFHGKTRREQEALRLLPPETGLFLVRESNTNPGDYVLCVSFRDV 126

QY 167 HYRVLHRDGHLTIDEAVFFCNLMDMVHYSKDKGAICTKLYRKPKRGTKSAEELARA 226
 127 EHRYIMHASKLUSIDEEVYFENIMLQMVLYHPTSDADGLCIRLKPMEGTVAQDEFYRS 186

QY 227 GWLNLOHLTGAQIGEFGAVLQGEVLQGKQAVKNIKCDTAQAFDETAMTKMHE 286
 187 GWALNMKELKLQITGKGEFGDVMGLGDYRGNKAVKCTKINDATAQAFLAESTMQLRHS 246

QY 287 NIVRLIGVILHQ-GLYTIVMHEVSKGNIVNLFTRGRALVNTAQQLQSLHVAEGMYLE 344
 247 NIVQOLIGVIVEKGGLYVTEMAKSLVYDYLRSGRVSLGQCLKSLDVCEAMEYLE 306

QY 345 SKRLVHDLAARNILVSEDLVAKVSDRGLAKAERKGKGLDSSRLPVKWTAPEALKHGKFTSK 404
 307 GNNFVHRDLAARNVLVSEDNVAKVSDFGLTKEASSTQDTGKLPVKWTAPEALKFSTK 366

QY 405 SDWWSFGVLLMEVFSGRVPPYPRIPKDVYPRVEKGYKMDADPGCPPAVYEVNKNCHLD 464
 367 SDWWSFGVLLMEVFSGRVPPYPRIPKDVYPRVEKGYKMDADPGCPPAVYEVNKNCHLD 426

QY 465 PARRPPFKLAEL 478
 Db 427 AAMRPSFLQLRQL 440

APPLICANT: Meric, Funda
 APPLICANT: Saini, Alysequil
 APPLICANT: Mills, Gordon B.
 TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT, FILE REFERENCE: MRT-038
 CURRENT APPLICATION NUMBER: US10/177,293
 CURRENT FILING DATE: 2002-06-21
 PRIORITY NUMBER: US 60/299,887
 PRIORITY NUMBER: US 60/301,572
 PRIORITY NUMBER: US 60/362,585
 PRIORITY FILING DATE: 2001-06-27
 PRIORITY APPLICATION NUMBER: US 60/306,501
 PRIORITY FILING DATE: 2001-07-18
 PRIORITY APPLICATION NUMBER: US 60/325,002
 PRIORITY FILING DATE: 2001-09-25
 PRIORITY APPLICATION NUMBER: US 60/301,572
 PRIORITY FILING DATE: 2002-03-05
 PRIORITY APPLICATION NUMBER: US 60/xxxx,xxx
 PRIORITY FILING DATE: 2002-05-14
 NUMBER OF SEQ ID NOS: 505
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 88
 LENGTH: 450
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-177-293-88

Query Match 46.6%; Score 1245.5; DB 15; Length 450;
 Best Local Similarity 54.1%; Pred. No. 4.4e-93; Matches 235; Conservative 81; Mismatches 115; Indels 3; Gaps 2;

QY 47 WAPGTOCITKCEHTRPKPGELAFRKGDVWVILEACENKSWYRKHHTSGOEGLLAAGAIR 106
 Db 8 WPSGTECIAKYNFHGTAEQDLFCKGVDLTVAVTKDPWYKAKNV-GREGITIPANVQ 66

QY 107 EREALSADPKLSLMPWFGKISGOAVQOLQPPEGLFVYRESARHPGYVLCISFGD 166
 Db 67 KREGVKGAKTKLSLMPWFGKTRDQAERLILYPPETGLFLVRESTRNYPGDTYLCVSCDGK 126

QY 167 IHYRLHROGLHTIDEAVFCNLMDVENEYHSDKGAICTKLVRKRKHGTSAEELARA 226
 Db 127 EHRYMHASKLSDEEVYFENLMLVENEHTSDAGLICRILIKVMEGTVAADEFYRS 186

QY 227 GWLNLQHLTGAQOIGEGFAGVQYLGKQVAKNKTQDGLKPVWTAPEALRKFSK 186
 Db 187 GWALMKELKLQQTGKGFGDVMGQYKAVKCIKNDATAQAFLAESYMTOLRHS 246

QY 287 NLVRLGVLHQ--GLTYMEHVSKGNLNFRGRJALNTQDLSLHVAGEMEY 344
 Db 247 NWOLLGIVTEEKGGLYIVTEYMAKGSVLYDLRSRGSRLGDCILKSFSDVCEAMEYLE 306

QY 345 SKKLVHDLAARNLIVSLEDLVAKVSDFGLAKAERKGSLPSRLPKWTAPEALKFKSTK 404
 Db 307 GNNFHRDLAARNLIVSLEDLVAKVSDFGLAKAERKGSLPSRLPKWTAPEALKFKSTK 366

QY 405 SDVNSFGVLLWEVTSYGRADYPKMSLKEYSEAVGYRMEPPEGCPGPVHLMSSWEA 464
 Db 367 SDVNSFGILWELTSFGRVYPRFLKDWPVPRVEGYKMDAPDGCPPAVYEVMKNCWHLID 426

QY 465 PARRPFRLAELK 478
 Db 427 AAMRPSFLQLOREQL 440

RESULT 9
 US-10-288-377A-2
 Sequence 2 Application US10298377A
 Publication No. US20030130209A1
 GENERAL INFORMATION:
 APPLICANT: The Scripts Research Institute
 APPLICANT: Chereh, David A.
 APPLICANT: Paul, Robert

APPLICANT: Eliceiri, Brian
 TITLE OF INVENTION: Method of treatment of Myocardial Infarction
 FILE REFERENCE: TSRT-651.5
 CURRENT APPLICATION NUMBER: US10/298,377A
 CURRENT FILING DATE: 2002-11-18
 PRIORITY NUMBER: 10/298,377
 PRIORITY NUMBER: 09/470,881
 PRIORITY NUMBER: 1999-12-22
 PRIORITY NUMBER: 09/338,248
 PRIORITY FILING DATE: 2000-03-29
 PRIORITY APPLICATION NUMBER: PCT/US99/11780
 PRIORITY FILING DATE: 1999-05-28
 PRIORITY APPLICATION NUMBER: 60/087,220
 PRIORITY FILING DATE: 1998-05-29
 NUMBER OF SEQ ID NOS: 4
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 2
 LENGTH: 450
 TYPE: PRT
 ORGANISM: homo sapiens
 US-10-298-377A-2

Query Match 46.6%; Score 1245.5; DB 16; Length 450;
 Best Local Similarity 54.1%; Pred. No. 4.4e-93; Matches 235; Conservative 81; Mismatches 115; Indels 3; Gaps 2;

QY 47 WAPGTOCITKCEHTRPKPGELAFRKGDVWVILEACENKSWYRKHHTSGOEGLLAAGAIR 106
 Db 8 WPSGTECIAKYNFHGTAEQDLFCKGVDLTVAVTKDPWYKAKNV-GREGITIPANVQ 66

QY 107 EREALSADPKLSLMPWFGKISGOAVQOLQPPEGLFVYRESARHPGYVLCISFGD 166
 Db 67 KREGVKGAKTKLSLMPWFGKTRDQAERLILYPPETGLFLVRESTRNYPGDTYLCVSCDGK 126

QY 167 IHYRLHROGLHTIDEAVFCNLMDVENEYHSDKGAICTKLVRKRKHGTSAEELARA 226
 Db 127 EHRYMHASKLSDEEVYFENLMLVENEHTSDAGLICRILIKVMEGTVAADEFYRS 186

QY 227 GWLNLQHLTGAQOIGEGFAGVQYLGKQVAKNKTQDGLKPVWTAPEALRKFSK 186
 Db 187 GWALMKELKLQQTGKGFGDVMGQYKAVKCIKNDATAQAFLAESYMTOLRHS 246

QY 287 NLVRLGVLHQ--GLTYMEHVSKGNLNFRGRJALNTQDLSLHVAGEMEY 344
 Db 247 NWOLLGIVTEEKGGLYIVTEYMAKGSVLYDLRSRGSRLGDCILKSFSDVCEAMEYLE 306

QY 345 SKKLVHDLAARNLIVSLEDLVAKVSDFGLAKAERKGSLPSRLPKWTAPEALKFKSTK 404
 Db 307 GNNFHRDLAARNLIVSLEDLVAKVSDFGLAKAERKGSLPSRLPKWTAPEALKFKSTK 366

QY 405 SDVNSFGVLLWEVTSYGRADYPKMSLKEYSEAVGYRMEPPEGCPGPVHLMSSWEA 464
 Db 367 SDVNSFGILWELTSFGRVYPRFLKDWPVPRVEGYKMDAPDGCPPAVYEVMKNCWHLID 426

QY 465 PARRPFRLAELK 478
 Db 427 AAMRPSFLQLOREQL 440

RESULT 10
 US-09-928-266-9
 Sequence 9 Application US09929266
 Publication No. US2003004594A1
 GENERAL INFORMATION:
 APPLICANT: Brian T. Chait
 APPLICANT: Dafin R. Latimer
 APPLICANT: Paul M. Lizardi
 APPLICANT: Eric R. Kershner
 APPLICANT: Jon S. Morrow
 APPLICANT: Matthew E. Roth
 APPLICANT: Martin J. Mattessich

APPLICANT: Kevin J. McConnell
 TITLE OF INVENTION: ULTRA-SENSITIVE DETECTION SYSTEMS
 FILE REFERENCE: 01173.000302

CURRENT APPLICATION NUMBER: US/09/929,266
 CURRENT FILING DATE: 2001-08-13
 PRIOR APPLICATION NUMBER: 2000-08-11

PRIOR APPLICATION NUMBER: 60/283,498
 PRIOR FILING DATE: 2000-04-12

NUMBER OF SEQ ID NOS: 33
 SOFTWARE: FastSEQ fcc Windows Version 4.0

SEQ ID NO: 9
 LENGTH: 357
 TYPE: PRT

ORGANISM: Homo sapiens

US-09-929-266-9

Query Match 34.3%; Score 916; DB 11; Length 357;
 Best Local Similarity 52.3%; Pred. No. 2a-66; Mismatches 97; Indels 8; Gaps 3;
 Matches 183; Conservative 62; Pred. No. 2a-66; Mismatches 97; Indels 8; Gaps 3;

Qy 47 WAPGTCQCTKCEHTRPKPGLAFRKQDVNTILEACENKSWYRKHHTSGOEGILAACLR 106
 Db 8 WPSGTECIAKYNHGTAEQDLPCKGQDVNTIAVTKDOPENWYAKNVY-GREGITPANVQ 66

Qy 107 EREALSADPKLSLMPWFGKISQEAQVQLQQPEDGLFLVRESARHPCDDYVLCVSFRDV 166
 Db 67 KREGVKAGTKLSLMPWFGKTRREQAERLPLYPETGFLFLVRESTDNYPGDYTLCVSCDGKV 126

Qy 167 IHWVVLHRDGHLTIDEAVFCNLMDMVEHYSKDKRGAICTKLYVRPKRKHGKTAEEELARA 226
 Db 127 EHRYTMTHASKLUSLDPYENMOLVEHYTSADGLCTRLIKPKMEGTVAAQDEYRS 186

Qy 227 GWLNLNQHILTGQOIGEFGAVLQGEYLGQKAVAKNPKCDTAQAFDDETAVMKHHE 286
 Db 187 GWAALNKELKLLOTIGKEFGDVLGDXRGRKNAVKCIKNDTAQATLAESVMTQHHS 246

Qy 287 NLVRLGVTILHQ--GLYTMEHVSKGNLNFLTRGRALVNTAQLQFLSLRVAEQMEYLE 344
 Db 247 NLVQVLGVTIVEEKGLYLVTEXMAKGSVLDSRSGRSVLGGDCCLKFLSDVCEAMEYLE 306

Qy 345 SKVLVHDLAARNLIVSLDVLAKVSDGLAK---ERKGDDSRPKV 389
 Db 307 GNNFVHRDLAARNLIVSLDVLAKVSDGLAK---ERKGDDSRPKV 356

RESULT 11
 US-09-840-704-3
 Sequence 3, Application US/09840704

PATENT INFORMATION:
 APPLICANT: Dechar, Shoukat
 TITLE OF INVENTION: Intergrin-Linked Kinase and its Uses
 FILE REFERENCE: KIN-2C0N
 CURRENT APPLICATION NUMBER: US/09/840,704
 CURRENT FILING DATE: 2001-04-23
 PRIOR APPLICATION NUMBER: 09/556,906
 PRIOR FILING DATE: 2000-05-09

PRIOR APPLICATION NUMBER: US/08/7752,345
 PRIOR FILING DATE: 1996-11-19
 NUMBER OF SEQ ID NOS: 16
 SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO: 3
 LENGTH: 258
 TYPE: PRT

ORGANISM: H. sapiens
 FEATURE:
 NAME/KEY: Other
 LOCATION: (1)...(258)
 US-09-840-704-3

Query Match 28.8%; Score 768; DB 10; Length 258;
 US-09-977-269-18

Query Match 27.8%; Score 742.5; DB 9; Length 509;
 Best Local Similarity 37.6%; Pred. No. 4e-52; Mismatches 161; Conservative 87; Mismatches 155; Indels 25; Gaps 9;

Matches 161; Conservative 87; Mismatches 155; Indels 25; Gaps 9;

Qy 65 GELAFRKGDVNTILEACENKSWYRKHHTSGOEGILAACLR 124
 Db 78 GDLGFRKEQRLTLE--OSGENWKAQSLTGGFIPFNFVAKANLEPE----PWFF 129

Qy 125 GKSQGAVQQLQPPEDGLFLVRECARHPCDDYVLCVSFRDV 176
 Db 130 KHLRKDAERQQLAGPWHGSLRLEESTAGSFSLSVRQDQDQEVKVKYKIRLDNG 189

Qy 177 HLTTIDEAVFCNLMDMVEHYSKDKRGAICTKLYVRPKRKHGKTSAAEELARASWLLNLQHLT 236
 Db 190 GFTISPRITFPGLHLYRHYTNAQDGLCTRSRPG---TORPKDWWEDEWVPRTELK 246

Qy 237 LGAQIGEFGAVLQGEYLGQKAVAKNPKCDTAQAFDDETAVMKHHE 294
 Db 247 LVERGAGOFGEVWMGYNGHVKVAKSLKOGSMSDAFLAEANLKOLOHLVRLYV 306

Qy 295 IHLQGLITVMEHVSKGNLNFLTRGRALVNTAQLQFLSLRVAEQMEYLEKRLVIRLDA 354
 Db 307 VTOEPVITVEMENGSVLDLKTPSGKLTINKLDMAQIAEGMIFIERNYIIRDLR 366

Qy 355 ARNLVSEEDLVAKVSDGLAKA---ERKGDDSRPKVWPEAKRKGKTTKSWSF 410
 Db 367 AANILVSDTLSCKIADGLGLRJEDNEYTAREGAKFPIKWTAPAEANIYGTPIKSDVWSF 426

Best Local Similarity 58.8%; Pred. No. 1.4e-54;
 Matches 147; Conservative 45; Mismatches 56; Indels 2; Gaps 1;

Matches 147; Conservative 45; Mismatches 56; Indels 2; Gaps 1;

Qy 231 NLOQHTLGAQIGEFGAVLQGEYLGQKAVAKNPKCDTAQAFDDETAVMKHHE 290
 Db 1 NMKEKLQIQTICKGEFSYMLQDYGKAVAKCIKUDATAQFLAEASVMTQHNLVR 60

Qy 291 LIGVILHQ--GLYIVMEHVSKGNLNLTRGRALVNTAQLQFLSLRVAEQMEYLESKKL 348
 Db 61 LIGVTEVEKGGLYLVTEYMAKGSVLDSRSGRSVLGGDCCLIKFSLDVCEAMEYLSNNF 120

Qy 349 VHRDLAARNLIVSLDVLAKVSDGLAKAERKGDDSRPKV 408
 Db 121 VHRDLAARNLIVSLDVLAKVSDGLAKAERKGDDSRPKV 408

Qy 409 SPCVLUHNEVFSYGRPKMSKREVSIAVKEGRYMRPEGGCPGPVHLMSSCWEAPARR 468
 Db 181 SFGILLWELYSFGVPRIPRIPKDVVERVEKYMADPGCOPAVEVKNCWHLADR 240

Qy 469 PPFKLAELK 478
 Db 241 PSFLQRLQ 250

RESULT 12
 US-09-977-269-18

; Sequence 18, Application US/09977-269

; Patent No. US20020082037A1

; GENERAL INFORMATION:

; APPLICANT: ULLRICH, AXEL

; APPLICANT: GISHKOV, MIKHAIL

; APPLICANT: SURE, IRMINGARD

; TITLE OF INVENTION: NOVEL MEGAKARYOCYTIC PROTEIN TYROSINE KINASES

; FILE REFERENCE: 038602/1260

; CURRENT APPLICATION NUMBER: US/09/977, 269

; CURRENT FILING DATE: 2001-10-16

; PRIOR APPLICATION NUMBER: 08/232,545

; PRIOR FILING DATE: 1994-04-22

; NUMBER OF SEQ ID NOS: 24

; SOFTWARE: Patentin Ver. 2.1

; SEQ ID NO: 18

; LENGTH: 509

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-977-269-18

QY 411 GVLMEVFSYGRAPYRPMKSLKEVSEAVKGRMPEPGCPVHVLMSSCWEAEPARRP. 470
 ; GENERAL INFORMATION:
 ; APPLICANT: ULLRICH, AXEL
 ; APPLICANT: GISHIZKY, MIKHAIL
 ; APPLICANT: SURES, IRMINGARD
 ; TITLE OF INVENTION: NOVEL MEGAKARYOCYTIC PROTEIN TYROSINE KINASES
 ; FILE REFERENCE: 038602/1259
 ; CURRENT APPLICATION NUMBER: US/09/977,261
 ; CURRENT FILING DATE: 2001-10-16
 ; PRIOR APPLICATION NUMBER: 08/232,545
 ; PRIOR FILING DATE: 1994-04-22
 ; NUMBER OF SEQ ID NOS: 24
 ; SOFTWARE: Patentin Ver. 2.1
 ; SEQ ID NO 18
 ; LENGTH: 509
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-977-261-18

Query Match 27.8%; Score 742.5; DB 11; Length 509;
 Best Local Similarity 37.6%; Pred. No. 4e-52; Matches 161; Conservative 87; Mismatches 155; Indels 25; Gaps 9;
 Matches 161; Conservative 87; Mismatches 155; Indels 25; Gaps 9;

QY 65 GELAERKGDVVTILEACENKSWYRKHHSQEGGLAAGALRERALSADPKLSIMPWFH 124
 ;
 Db 78 GDLGFEKGEQIRILE-QSGEWKKAQSLTIGEFGTIPFWVAKANSLEPE-----PWFF 129
 ;
 QY 125 GKISEQEAVQOLQPED-GLFLVRESARAHGDYVLCV---SIGRDIHYRVLHD-G 176
 ;
 Db 130 KNLRSRDAEROLLAPOGNTGSSFLIRSESTAGSFSLSVRDFDQNGEVVVKHYKIRLDNG 189
 ;
 Qy 177 HLTIDBAVFFCNLMOMVHYSKDKAICTKLVRKRKGTKSAESELARAGWLNQHET 236
 ;
 Db 190 GFYISPRITFPGHLHVRHTNASDGLCTRSRQO---TOKPQFWWEDWEVRETLK 246
 ;
 Qy 237 LGAQIGEGERGAVLQYLG-KAVKVKNI-CDVTAQAFDETAWTMKOHENLVRLLGV 294
 ;
 Db 247 LVERLGAGQFGEVWKGYNGHTKAVKSLKQGSMSPDAFLAEANJMKQLOHQHORLVRLY 306
 ;
 Qy 295 ILHQGLYTVMRHVKSGNLVNLTRGRALYNTAQOLQFLHVAEGMEYLESSKKLVRHDLA 354
 ;
 Db 307 VTQEPYIYIYIYMENGSLVDFLKTSGIKLTINKLDMQAQIAEGMAFERNYIHRDLR 366
 ;
 Qy 355 ARNLIVSEDLIVAKVSDFLGAKA---ERKGIDSSSLVPUKMTAPEALKHGKFTSKSDWSE 410
 ;
 Db 367 AANLIVSDTSLCKIADFLGALARIEDNEYTAREGAKFPIKNTAPEAINYGTFTKSDWSE 426
 ;
 QY 411 GVLMEVFSYGRAPYRPMKSLKEVSEAVKGRMPEPGCPVHVLMSSCWEAEPARRP 470
 ;
 Db 427 GILLEIVTHGRIPPGMTNPEVIONLERGYRMVRPDNCPEELYOLMLRCWERPDRPT 486
 ;
 Qy 471 FRKLAEKL 478
 ;
 Db 487 FDYLRSVL 494

RESULT 13
 ; Sequence 18 Application US/09977260
 ; GENERAL INFORMATION:
 ; APPLICANT: ULLRICH, AXEL
 ; APPLICANT: GISHIZKY, MIKHAIL
 ; APPLICANT: SURES, IRMINGARD
 ; APPLICANT: SURES, IRMINGARD
 ; TITLE OF INVENTION: NOVEL MEGAKARYOCYTIC PROTEIN TYROSINE KINASES
 ; FILE REFERENCE: 038602/1260
 ; CURRENT APPLICATION NUMBER: US/09/977,260
 ; CURRENT FILING DATE: 2001-10-16
 ; PRIOR APPLICATION NUMBER: 08/232,545
 ; PRIOR FILING DATE: 1994-04-22
 ; NUMBER OF SEQ ID NOS: 24
 ; SOFTWARE: Patentin Ver. 2.1
 ; SEQ ID NO 18
 ; LENGTH: 509
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-977-261-18

Query Match 27.8%; Score 742.5; DB 11; Length 509;
 Best Local Similarity 37.6%; Pred. No. 4e-52; Matches 161; Conservative 87; Mismatches 155; Indels 25; Gaps 9;

QY 65 GELAERKGDVVTILEACENKSWYRKHHSQEGGLAAGALRERALSADPKLSIMPWFH 124
 ;
 Db 78 GDLGFEKGEQIRILE-QSGEWKKAQSLTIGEFGTIPFWVAKANSLEPE-----PWFF 129
 ;
 QY 125 GKISEQEAVQOLQPED-GLFLVRESARAHGDYVLCV---SIGRDIHYRVLHD-G 176
 ;
 Db 130 KNLRSRDAEROLLAPOGNTGSSFLIRSESTAGSFSLSVRDFDQNGEVVVKHYKIRLDNG 189
 ;
 Qy 177 HLTIDBAVFFCNLMOMVHYSKDKAICTKLVRKRKGTKSAESELARAGWLNQHET 236
 ;
 Db 190 GFYISPRITFPGHLHVRHTNASDGLCTRSRQO---TOKPQFWWEDWEVRETLK 246
 ;
 Qy 237 LGAQIGEGERGAVLQYLG-KAVKVKNI-CDVTAQAFDETAWTMKOHENLVRLLGV 294
 ;
 Db 247 LVERLGAGQFGEVWKGYNGHTKAVKSLKQGSMSPDAFLAEANJMKQLOHQHORLVRLY 306
 ;
 Qy 295 ILHQGLYTVMRHVKSGNLVNLTRGRALYNTAQOLQFLHVAEGMEYLESSKKLVRHDLA 354
 ;
 Db 307 VTQEPYIYIYMENGSLVDFLKTSGIKLTINKLDMQAQIAEGMAFERNYIHRDLR 366
 ;
 Qy 355 ARNLIVSEDLIVAKVSDFLGAKA---ERKGIDSSSLVPUKMTAPEALKHGKFTSKSDWSE 410
 ;
 Db 367 AANLIVSDTSLCKIADFLGALARIEDNEYTAREGAKFPIKNTAPEAINYGTFTKSDWSE 426
 ;
 QY 411 GVLMEVFSYGRAPYRPMKSLKEVSEAVKGRMPEPGCPVHVLMSSCWEAEPARRP 470
 ;
 Db 427 GILLEIVTHGRIPPGMTNPEVIONLERGYRMVRPDNCPEELYOLMLRCWERPDRPT 486
 ;
 Qy 471 FRKLAEKL 478
 ;
 Db 487 FDYLRSVL 494

RESULT 14
 ; Sequence 18 Application US/09977261
 ; Publication No. US20030054527A1

RESULT 15
 ; Sequence 13 Application US/09977269
 ; General Information:
 ; Patient No. US20020082037A1
 ; APPLICANT: ULLRICH, AXEL
 ; APPLICANT: GISHIZKY, MIKHAIL
 ; APPLICANT: SURES, IRMINGARD
 ; TITLE OF INVENTION: NOVEL MEGAKARYOCYTIC PROTEIN TYROSINE KINASES
 ; FILE REFERENCE: 038602/1260
 ; CURRENT APPLICATION NUMBER: US/09/977,269
 ; PRIOR APPLICATION NUMBER: 08/232,545
 ; PRIOR FILING DATE: 1994-04-22
 ; NUMBER OF SEQ ID NOS: 24
 ; SOFTWARE: Patentin Ver. 2.1
 ; LENGTH: 536
 ; SEQ ID NO 13

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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-977-269-13

Query Match 27.2%; Score 727; DB 9; Length 536;
Best Local Similarity 35.2%; Pred. No. 7.8e-51;
Matches 182; Conservative 83; Mismatches 178; Indels 74; Gaps 14;

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Qy 37 PVSA---RMPTRRWAP-----GTOCITKCEHTRPKPG----- 65
Db 41 PASADCHRGPSAAFAAAEPKLRGGFNSSDTVISPQRAGPLAGGYTTVALDYERSRTE 100
Qy 66 -ELAFRKGVVTTILEACENKSWYRKKHHSQEGUAGALRERBALSADPKLUSLMPWPH 124
Db 101 TDLSFRKGGERLQIVNTEG-DWWLAAHSLSTGOTGYIPSNVAPSDSIQAE-----EWTF 153
Qy 125 GKIQSQEAQVQLQPPED-GFLFLYRESARHGPDYVLCVS---FGRDVHYRLHD-G 176
Db 154 GKTRRERSERULLNAENPRGTFLYRESEFTKGAVCLSVDFDNAGLNLKHYKIRKLDG 213
Qy 177 HLTIDBAVFFCNLMQDMEVHYSKDKGAICTKL-VRPKRKGTKSAAEEELARAGWLNLOH 234
Db 214 GFYITSRTQFNSLQOLVAVYKSHADGLCHRLTVQPTSKRQTOG---LAKDANEIPRES 269
Qy 235 LTIGAQIGEGESEFGAVLOGEIG-DRVAVNIK-GDVTAQAFLDPEAWMKMHOHENLYRL 292
Db 270 LRLEVKGQCGFGEVWMMGTTWRAKTLKPGTMSPEAFLOEQVMKRLRERKLVOLY 329
Qy 293 GVLHQGLYIVMERYHSKGNLVNFRLTRGRALVNTAQLOPSLHVAEGLYLESKLVHED 352
Db 330 AVVSEEPYIYTTEYMSKGSLIDFLKGETCYRLPQVLMQASGMAYVERMYVHD 389
Qy 353 LAARNILVSEDLVAKVSDGLAKA---PERKGLDSSRLPVWTAPEALHKGKFTSKSDW 408
Db 390 LRAANILVGENLNUCKVADGLARLIEDNEYTARQGAKFKWTAPEAALYGRFTIKSDW 449
Qy 409 SFGVILWEEVSYGRAPYKHSILKEYSEAVERGYRNEPPGCPGPVPHVLLSSCWAEPAR 468
Db 450 SFGIILLTETLTKGRVYPPGVNREVDQVERGYRMPCPBPCPESLHDIMQCWRKEPEER 509
Qy 469 PPFRLKLAEKARELJSAGAIPASVSCQDAGSTSRSQ 505
Db 510 PTFEYLOAFL-----EDYFNSTEPOYQ 531

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Search completed: July 29, 2003, 09:53:36
 Job time : 29 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 29, 2003, 09:49:12 ; Search time 20 Seconds
(without alignments)
1072.580 Million cell updates/sec

Title: US-09-977-261-2
Perfect score: 2671
Sequence: 1 MAGRGLSVWRAGFHGCDSAE....., PASVSGQDADGSTSPRSQEP 507

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*

1: /cgn2_6/ptodata/1/iaa/5a_COMB_pep: *
2: /cgn2_6/ptodata/1/iaa/5b_COMB_pep: *
3: /cgn2_6/ptodata/1/iaa/6a_COMB_pep: *
4: /cgn2_6/ptodata/1/iaa/6b_COMB_pep: *
5: /cgn2_6/ptodata/1/iaa/PCMS_COMB_pep: *
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	2671	100.0	507	4	US-08-426-509A-2
2	2671	100.0	507	4	US-08-422-545-2
3	2671	100.0	507	5	PCP-US95-05008-2
4	2664	99.7	507	2	US-08-604-988A-5
5	2645	91.5	527	4	US-09-315-920-2
6	2444	91.5	466	2	US-08-604-988A-4
7	2434.5	91.1	528	2	US-08-876-882-2
8	2012	75.3	386	4	US-09-741-154-4
9	2012	75.3	415	4	US-09-741-154-2
10	1269	47.5	246	2	US-08-604-988A-3
11	1245.5	46.6	450	4	US-08-426-509A-7
12	1245.5	46.6	450	4	US-08-432-505-7
13	1245.5	46.6	450	5	PCP-US95-05008-7
14	797	29.8	269	2	US-08-426-509A-35
15	768	28.8	258	3	US-09-035-705-3
16	768	28.8	258	3	US-08-955-841-3
17	768	28.8	258	4	US-09-390-425-3
18	768	28.8	258	4	US-09-566-906-3
19	742.5	27.8	509	3	US-09-039-558B-17
20	742.5	27.8	509	4	US-08-426-509A-18
21	742.5	27.8	509	4	US-09-457-040B-8
22	742.5	27.8	509	4	US-08-232-545-18
23	742	27.8	509	5	PCP-US95-05008-18
24	732	27.4	533	1	US-07-830-011A-2
25	732	27.4	533	5	PCP-US93-0445-2
26	727	27.2	536	1	US-07-830-011A-4
27	727	27.2	536	4	US-08-426-509A-13

ALIGMENTS

28	727	27.2	536	4	US-08-232-545-13	Sequence 13, Appl
29	727	27.2	536	5	PCP-US93-00445-14	Sequence 4, Appl
30	727	27.2	536	5	PCP-US95-05008-13	Sequence 13, Appl
31	720.5	27.0	505	4	US-08-426-509A-17	Sequence 17, Appl
32	720.5	27.0	505	4	US-08-232-545-17	Sequence 17, Appl
33	720.5	27.0	505	5	PCP-US95-05008-17	Sequence 17, Appl
34	710	26.6	543	4	US-08-426-509A-14	Sequence 14, Appl
35	710	26.6	543	4	US-08-232-545-14	Sequence 14, Appl
36	710	26.6	513	5	PCP-US95-05008-14	Sequence 15, Appl
37	707	26.5	512	4	US-08-426-509A-16	Sequence 16, Appl
38	707	26.5	512	4	US-08-232-545-16	Sequence 16, Appl
39	707	26.5	512	5	PCP-US95-05008-16	Sequence 16, Appl
40	699.5	26.2	536	4	US-08-426-509A-12	Sequence 12, Appl
41	699.5	26.2	536	4	US-08-232-545-12	Sequence 12, Appl
42	699.5	26.2	536	5	PCP-US95-05008-12	Sequence 12, Appl
43	699	26.2	499	4	US-08-426-509A-19	Sequence 19, Appl
44	699	26.2	499	4	US-08-232-545-19	Sequence 19, Appl
45	699	26.2	499	5	PCP-US95-05008-19	Sequence 19, Appl

RESULT 1

US-08-426-509A-2

; Sequence 2, Application US/08426509A
; Patent No. 6326469

GENERAL INFORMATION:

APPLICANT: Ulrich, Axel

APPLICANT: Gishizky, Mikhail

APPLICANT: Suresh, Iman G.

TITLE OF INVENTION: NOVEL MEGAKARYOCYTIC PROTEIN

TITLE OF INVENTION: TYROSINE KINASES

NUMBER OF SEQUENCES: 21

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York,

STATE: NY

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/426,509A

FILING DATE: 21-APR-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/232,545

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Cozzoli, Laura A

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 7683-0074-999

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-790-9090

TELEFAX: 212-869-9741

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 507 amino acids

TYPE: amino acid

STRANDEDNESS: unknown

TOPOLOGY: unknown

MOLECULE TYPE: No. 6326469e

US-08-426-509A-2

Query Match Best Local Similarity 100.0%; Score 2671; DB 4; Length 507; Matches 507; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MAGRGLSVWRAFHGCQSAELPRVSPFLRHWPPVSAAMPTRWRAPGCTICKE 60
 1 MAGRGLSVWRAFHGCQSAELPRVSPFLRHWPPVSAAMPTRWRAPGCTICKE 60
 61 RPKPGELAFRKGDVVTILEACENSKWVTKHPSQEGLLAGALREREALSADPKLSM 120
 61 RPKPGELAFRKGDVVTILEACENSKWVTKHPSQEGLLAGALREREALSADPKLSM 120
 121 PWFHGKISQGAEVQQLQPPEDGFLVRESARHGDYVLCYSGFRDVTYVRLHDGHTI 180
 121 PWFHGKISQGAEVQQLQPPEDGFLVRESARHGDYVLCYSGFRDVTYVRLHDGHTI 180
 181 DAEVFFCNLMQDVEHYSKDKGAICTKLVPRKRHGKTSAAELRAGWLNLQHLTGQ 240
 181 DAEVFFCNLMQDVEHYSKDKGAICTKLVPRKRHGKTSAAELRAGWLNLQHLTGQ 240
 241 IGEGERGAVLQGEYLGOKVAKNICKDVTQAOFLDETAVMKMOHENLYRLGVLHQL 300
 241 IGEGERGAVLQGEYLGOKVAKNICKDVTQAOFLDETAVMKMOHENLYRLGVLHQL 300
 241 IGEGERGAVLQGEYLGOKVAKNICKDVTQAOFLDETAVMKMOHENLYRLGVLHQL 300
 301 YIVMEHVKSGNLYNLFRTGRALVNTAQOLQFSLHVAEGMEYLESKKLVHDLAARNLV 360
 301 YIVMEHVKSGNLYNLFRTGRALVNTAQOLQFSLHVAEGMEYLESKKLVHDLAARNLV 360
 361 SEDLVAKVSDGLAKERKGKGSRLPKWTAPEALKHGKFTSKDWSFGVLLWEFSY 420
 361 SEDLVAKVSDGLAKERKGKGSRLPKWTAPEALKHGKFTSKDWSFGVLLWEFSY 420
 421 GRAPYKMSLKEVSEAVEKGYRMEPPECGCPGPVHLMSSCWEAPRPPRKLAKLAR 480
 421 GRAPYKMSLKEVSEAVEKGYRMEPPECGCPGPVHLMSSCWEAPRPPRKLAKLAR 480
 481 ELRSAAGAPASVSGQDADGSTSPRSQEP 507
 481 ELRSAAGAPASVSGQDADGSTSPRSQEP 507
 RESULT 2
 US-08-232-545-2
 ; Sequence 2, Application US/08232545
 ; Patent No. 6506578
 ; GENERAL INFORMATION:
 ;
 APPLICANT: Gislizky, Axel
 APPLICANT: Sures, Iman G
 TITLE OF INVENTION: No. 6506578el Megakaryocytic Protein Tyrosine
 NUMBER OF SEQUENCES: 21
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Pennie & Edmonds
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: U.S.A.
 ZIP: 10036
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/232,545
 FILING DATE: 22-APR-1994
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Goruzzi, Laura A.
 REGISTRATION NUMBER: 30,742
 REFERENCE/DOCKET NUMBER: 7683-050
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212)790-9090
 TELEFAX: (212)869-9741
 TELEX: 66141 PENNIE
 RESULT³
 PCT-US95-05008-2
 ; Sequence 2, Application PC/US9505008
 ; GENERAL INFORMATION:
 ;
 APPLICANT: Sugen, Inc.
 APPLICANT: 515 Galveston Drive
 APPLICANT: Redwood City, California 94063-4720
 APPLICANT: United States of America
 APPLICANT: Wissenschaften E.V.
 APPLICANT: Hofgarten Str. 2
 APPLICANT: München 80539
 APPLICANT: Germany
 TITLE OF INVENTION: Novel Megakaryocytic Protein Tyrosine
 TITLE OF INVENTION: Kinases
 NUMBER OF SEQUENCES: 21
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Pennie & Edmonds
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: U.S.A.
 ZIP: 10036
 COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 FILING DATE: 24-APR-1995
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Coruzzi, Laura A.
 REGISTRATION NUMBER: 30,742
 REFERENCE/DOCKET NUMBER: US 08/232,545
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 790-9090
 TELEFAX: (212) 869-9741
 TELEX: 66141 PENNIE
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 507 amino acids
 TYPE: amino acid
 STRANDEDNESS: unknown
 TOPOLOGY: unknown
 MOLECULE TYPE: protein
 PCT-US95-05008-2

Query Match 100.0%: Score 2671; DB 5; Length 507;
 Best Local Similarity 100.0%; Pred. No. 2,7e-219; Mismatches 507; Conservative 0; Indels 0; Gaps 0;
 QY 1 MAGRGLSVSRAFGCDSAAELPRVSPRLRAWHPPVSPARMPTTRWAPGTCITKCEHT 60
 Db 1 MAGRGLSVSRAFGCDSAAELPRVSPRLRAWHPPVSPARMPTTRWAPGTCITKCEHT 60

QY 61 RPKGELAFRKGDVVTLACENKSWYRKHHTSGOEGLLAAGALRERDALSADPKLSM 120
 Db 61 RPKGELAFRKGDVVTLACENKSWYRKHHTSGOEGLLAAGALRERDALSADPKLSM 120

QY 121 PWFHGKISQEAQVQOLQPPEDGLFLVRESARHPGDYVLCVSFGRDVIVHVRVLRGHTI 180
 Db 121 PWFHGKISQEAQVQOLQPPEDGLFLVRESARHPGDYVLCVSFGRDVIVHVRVLRGHTI 180

QY 181 DEAVFFCNLMDMVEHYSKKGAICTKLVPRKRKGTKSAAELRAGWLNQLQHTGQ 240
 Db 181 DEAVFFCNLMDMVEHYSKKGAICTKLVPRKRKGTKSAAELRAGWLNQLQHTGQ 240

QY 241 IGEGEFGAVLQGEYLGQKAVKNIKCDVTAQAFQALDETAWTKMOKENLVRLLGVTLHQL 300
 Db 241 IGEGEFGAVLQGEYLGQKAVKNIKCDVTAQAFQALDETAWTKMOKENLVRLLGVTLHQL 300

QY 301 YIVMHEVSKGNLNVNLRTRGALVNTAQIQLQFSHLVAEGMEYLESKKLVHDLARNILV 360
 Db 301 YIVMHEVSKGNLNVNLRTRGALVNTAQIQLQFSHLVAEGMEYLESKKLVHDLARNILV 360

QY 361 SEDLVAKVQDFGLAKAERKGDSLRPVWTAPEALKKGFTSKSDWMSFGVLLWEVFSY 420
 Db 361 SEDLVAKVQDFGLAKAERKGDSLRPVWTAPEALKKGFTSKSDWMSFGVLLWEVFSY 420

QY 421 GRAPYPKMSLKEVSEAVEGYMRPEPGCPVHLMSSCWEAEPARRPPFRKLAELKAR 480
 Db 421 GRAPYPKMSLKEVSEAVEGYMRPEPGCPVHLMSSCWEAEPARRPPFRKLAELKAR 480

QY 481 ELRSAGAPASVSGDADGSTSPRSQEP 507
 Db 481 ELRSAGAPASVSGDADGSTSPRSQEP 507

RESULT 4
 US 08-604-989A-5
 ; Sequence 5, Application US/08604989A

Patent No. 5834208
 GENERAL INFORMATION:
 APPLICANT: Sakano, S.
 TITLE OF INVENTION: No. 5834208e1 Tyrosine Kinase
 NUMBER OF SEQUENCES: 11
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Pennie & Edmonds LLP
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: USA
 ZIP: 10036-2711
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSEQ Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/604,989A
 FILING DATE: February 23, 1996
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Charles E. Miller
 REGISTRATION NUMBER: 24,756
 REFERENCE/DOCKET NUMBER: 1920-026
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 790-9090
 TELEFAX: (212) 869-8664/9741
 TELEX: 66141 PENNIE
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 507 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 ORIGIN: human
 ORGANISM: human
 STRAIN: UT-7
 US-08-604-989A-5

Query Match 99.8%: Score 2664; DB 2; Length 507;
 Best Local Similarity 99.8%; Pred. No. 1e-218; Mismatches 506; Conservative 0; Indels 0; Gaps 0;
 QY 1 MAGRGLSVSRAFGCDSAAELPRVSPRLRAWHPPVSPARMPTTRWAPGTCITKCEHT 60
 Db 1 MAGRGLSVSRAFGCDSAAELPRVSPRLRAWHPPVSPARMPTTRWAPGTCITKCEHT 60

QY 61 RPKGELAFRKGDVVTLACENKSWYRKHHTSGOEGLLAAGALRERDALSADPKLSM 120
 Db 61 RPKGELAFRKGDVVTLACENKSWYRKHHTSGOEGLLAAGALRERDALSADPKLSM 120

QY 121 PWFHGKISQEAQVQOLQPPEDGLFLVRESARHPGDYVLCVSFGRDVIVHVRVLRGHTI 180
 Db 121 PWFHGKISQEAQVQOLQPPEDGLFLVRESARHPGDYVLCVSFGRDVIVHVRVLRGHTI 180

QY 181 DEAVFFCNLMDMVEHYSKKGAICTKLVPRKRKGTKSAAELRAGWLNQLQHTGQ 240
 Db 181 DEAVFFCNLMDMVEHYSKKGAICTKLVPRKRKGTKSAAELRAGWLNQLQHTGQ 240

QY 241 IGEGEFGAVLQGEYLGQKAVKNIKCDVTAQAFQALDETAWTKMOKENLVRLLGVTLHQL 300
 Db 241 IGEGEFGAVLQGEYLGQKAVKNIKCDVTAQAFQALDETAWTKMOKENLVRLLGVTLHQL 300

QY 301 YIVMHEVSKGNLNVNLRTRGALVNTAQIQLQFSHLVAEGMEYLESKKLVHDLARNILV 360
 Db 301 YIVMHEVSKGNLNVNLRTRGALVNTAQIQLQFSHLVAEGMEYLESKKLVHDLARNILV 360

QY 361 SEDLVAKVQDFGLAKAERKGDSLRPVWTAPEALKKGFTSKSDWMSFGVLLWEVFSY 420
 Db 361 SEDLVAKVQDFGLAKAERKGDSLRPVWTAPEALKKGFTSKSDWMSFGVLLWEVFSY 420

QY 421 GRAPYPKMSLKEVSEAVEGYMRPEPGCPVHLMSSCWEAEPARRPPFRKLAELKAR 480
 Db 421 GRAPYPKMSLKEVSEAVEGYMRPEPGCPVHLMSSCWEAEPARRPPFRKLAELKAR 480

QY 481 ELRSAGAPASVSGDADGSTSPRSQEP 507
 Db 481 ELRSAGAPASVSGDADGSTSPRSQEP 507

RESULT 5
US-09-315-928-2
; sequence 2, Application US/09315928
; patent No. 5365796

GENERAL INFORMATION:
; APPLICANT: Avraham, Hava
; TITLE OF INVENTION: METHODS OF DETECTION AND TREATMENT OF
; FILE REFERENCE: NEDH97-01PAZ
; CURRENT APPLICATION NUMBER: US/09/315, 928
; CURRENT FILING DATE: 1999-03-20
; PRIORITY APPLICATION NUMBER: US 08/876, 882
; PRIORITY FILING DATE: 1997-06-16
; PRIORITY APPLICATION NUMBER: US 60/035, 228
; PRIORITY FILING DATE: 1997-01-08
; NUMBER OF SEQ ID NBS: 5
; SOFTWARE: FAST-SEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 527
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-315-928-2

Query Match 91.5%; Score 2445; DB 4; Length 527;
Best Local Similarity 93.5%; Pred. No. 4.9e-200; Matches 472; Conservative 1; Mismatches 18; Indels 14; Gaps 2;

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1 MAGRSGLSWRAFHGCDSAELPRSPRLRAMPYSPARMPPRWRAGTQCTKCE 60
1 MAGRSGLSWRAFHGCDSAELPRSPRLRAMPYSPARMPPRWRAGTQCTKCE 60
61 RPKRGEELAFRKGDVTILEACENKSWYRKHHTSGQEGGLAAGALARREAL 60
61 RPKRGEELAFRKGDVTILEACENKSWYRKHHTSGQEGGLAAGALARREAL 60
61 RPKRGEELAFRKGDVTILEACENKSWYRKHHTSGQEGGLAAGALARREAL 60
61 RPKRGEELAFRKGDVTILEACENKSWYRKHHTSGQEGGLAAGALARREAL 60
121 PWRHKTSQEAQVQOLQPPEDGLFLVRESARHPGDYVLCVSGRDIHYRVLRGHTI 180
121 PWRHKTSQEAQVQOLQPPEDGLFLVRESARHPGDYVLCVSGRDIHYRVLRGHTI 180
181 DEAVFCNLMDYEHYSKDKGAICTKLYRPRKRKGHTKSAEEELARAGWILNQHILGAQ 240
181 DEAVFCNLMDYEHYSKDKGAICTKLYRPRKRKGHTKSAEEELARAGWILNQHILGAQ 240
241 IGEGEFGAVLQGEYLGOKVAVKNTKCDVTAQFLDETAVMTKOHENVLRLGVLHQL 300
241 IGEGEFGAVLQGEYLGOKVAVKNTKCDVTAQFLDETAVMTKOHENVLRLGVLHQL 300
241 IGEGEFGAVLQGEYLGOKVAVKNTKCDVTAQFLDETAVMTKOHENVLRLGVLHQL 300
301 YTMEVHVKRGNLYNRLTRGRALVNTAQLQFSLHVAEGMEYLESKKLVHDLAARNLY 360
301 YTMEVHVKRGNLYNRLTRGRALVNTAQLQFSLHVAEGMEYLESKKLVHDLAARNLY 360
361 SEDLWAKYKUSDFGLAKAERKGKLDSSRLPKWTAEEALKKFTSKDSWFGVILWESVY 420
361 SEDLWAKYKUSDFGLAKAERKGKLDSSRLPKWTAEEALKKFTSKDSWFGVILWESVY 420
421 GRAPYKPKSLKEYSEAVERKGYRMEPECGCPGPVHLMSSCWEAPRPPRKLAKLAR 480
421 GRAPYKPKSLKEYSEAVERKGYRMEPECGCPGPVHLMSSCWEAPRPPRKLAKLAR 480
420 GRAPYKPKSLKEYSEAVERKGYRMEPECGCPGPVHLMSSCWEAPPAGHP----- 469
481 ELSAGAPASVSGQDADSTPSQ 505
470 --- SANWPRSWPSGSYAVQVOPPSQ 491

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Query Match 91.5%; Score 2444; DB 2; Length 466;
Best Local Similarity 100.0%; Pred. No. 5e-200; Matches 466; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 42 MPTRWAPEGTQCTKCEHTTRPKPGLAFRKGDVTILEACENKSWYRKHHTSGQEGGLA 101
QY 1 MPTRWAPEGTQCTKCEHTTRPKPGLAFRKGDVTILEACENKSWYRKHHTSGQEGGLA 60
QY 102 AGALRREALSADPKLSLMWFHKTSQEAQVQOLQPPEDGLFLVRESARHPGDYVLCV 161
QY 61 AGALRREALSADPKLSLMWFHKTSQEAQVQOLQPPEDGLFLVRESARHPGDYVLCV 120
QY 162 FGRDVTYHYRVLRGHTIDEAVFCNLMDYEHYSKDKGAICTKLYRPRKRKGHTS 221
QY 121 FGRDVTYHYRVLRGHTIDEAVFCNLMDYEHYSKDKGAICTKLYRPRKRKGHTS 180
QY 222 ELARGWILNQHILGQIYGEGERGAVILOGEYLGOKVAVKNTKCDVTAQFLDETAVMT 281
QY 181 ELARGWILNQHILGQIYGEGERGAVILOGEYLGOKVAVKNTKCDVTAQFLDETAVMT 240
QY 282 KMQHENVLRLGVLHQLTQFSLHVAEGMEYLESKKLVHDLAARNLY 341
QY 241 KMQHENVLRLGVLHQLTQFSLHVAEGMEYLESKKLVHDLAARNLY 300
QY 342 YLESRKLVHDLAARNLYNRLTRGRALVNTAQLQFSLHVAEGME 401
QY 301 YLESRKLVHDLAARNLYNRLTRGRALVNTAQLQFSLHVAEGME 360
QY 402 TSKDWWSCWGLMVEFSGRAPPKMSLUKEVSEAVERKGYRMEPECGCPGPVHLMSSCWE 461

```

RESULT 6
US-08-604-989A-4
; Sequence 4, Application US/08604989A
; Patent No. 5834208
GENERAL INFORMATION:
; APPLICANT: Sakano, S.
; TITLE OF INVENTION: No. 5834208el Tyrosine Kinase
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 115 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FAST-SEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/604, 989A
; FILING DATE: February 23, 1996
; CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
; NAME: Charles E. Miller
; REGISTRATION NUMBER: 24,576
; REFERENCE/DOCKET NUMBER: 1920-026
TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864/9741
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 466 amino acids
; TYPE: amino acid
; TOPOLOGY: Linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: human
; STRAIN: UT-7
; US-08-604-989A-4

RESULT 7
 US-08-876-882-2
 ; Sequence 2, Application US/08876882
 ; Patent No. 5981201
 ; GENERAL INFORMATION:
 ; APPLICANT: Avraham, Hava
 ; APPLICANT: Groopman, Jerome E.
 ; TITLE OF INVENTION: METHODS OF DETECTION AND TREATMENT
 ; TITLE OF INVENTION: OF BREAST CANCER
 ; NUMBER OF SEQUENCES: 9
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Hamilton, Brook, Smith & Reynolds P.C.
 ; STREET: Two Militia Drive
 ; CITY: Lexington
 ; STATE: MA
 ; COUNTRY: USA
 ; ZIP: 02173-4799
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: Windows
 ; SOFTWARE: FastSEQ for Windows Version 2.0b
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/876, 882
 ; FILING DATE: 16-JUN-1997
 ; CLASSIFICATION: 435
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: 60/035, 228
 ; FILING DATE: 08-JAN-1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Doreen, Hogue M
 ; REFERENCE/DOCKET NUMBER: 36-361
 ; TELECOMMUNICATION INFORMATION:
 ; TELEFAX: 781-861-6240
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 528 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; FRAGMENT TYPE: internal
 ; US-08-876-882-2

Query Match Best Local Similarity 93.3%; Score 2434.5; DB 2; Length 528; Matches 472; Conservative 1; Mismatches 18; Indels 15; Gaps 3;

Qy 1 MAGRGSLSVSRRAFGCDSAAELPLRVSPPRFRAWHPPVPSARMPTTRWRAPGTOCTIKCET 60
 Qy 1 MAGRGSLSVSRRAFGCDSAAELPLRVSPPRFRAWHPPVPSARMPTTRWRAPGTOCTIKCET 60 .

Db 61 RPKPGELAFRKGDVVTLIEACENKSWYRKHHTSGQEGILAAAGALREREALSDAPKSL 119
 Db 61 RPKPGELAFRKGDVVTLIEACENKSWYRKHHTSGQEGILAAAGALREREALSDAPKSL 120

Qy 120 MPWFHKGKISQEAQVQLQPPEDGLFLVRESRARHPDGYVLCVSFGRDVTHYRVLHDHT 179
 121 MPWFHKGKISQEAQVQLQPPEDGLFLVRESRARHPDGYVLCVSFGRDVTHYRVLHDHT 180

Qy 180 IDEAVFFCNLMDMVHYSKDKGAICTKLRPKRKIGTKSAEELARAGMLNQHHTGA 239
 181 IDEAVFFCNLMDMVHYSKDKGAICTKLRPKRKIGTKSAEELARAGMLNQHHTGA 240

Db 361 VSDEDLVAKVSDFGGLAKAERKGLDSSRLPVKWTAPRALKHKGFTSDWVSGDFTSPRSQEP 507
 Db 421 EQLVAKVSDFGGLAKAERKGLDSSRLPVKWTAPRALKHKGFTSDWVSGDFTSPRSQEP 466

Db 301 LYIVMEHVSKGNLVNLTRGRALYNTAQOLOFSCHAVAEGLYMLSKKLYHRLDARNL 360

Qy 360 VSDEDLVAKVSDFGGLAKAERKGLDSSRLPVKWTAPRALKHKGFTSDWVSGDFTSPRSQEP 419
 Db 361 VSEDLVAKVSDFGGLAKAERKGLDSSRLPVKWTAPRALKHKGFTSDWVSGDFTSPRSQEP 419

Qy 300 LYIVMEHVSKGNLVNLTRGRALYNTAQOLOFSCHAVAEGLYMLSKKLYHRLDARNL 359

Db 420 YGRAPPKMSLKEVSEAVEKGYRMSPEPGCPGPVWVLMSSCWEARPPRPFKLAEKLA 479
 Db 420 YGRAPPKMSLKEVSEAVEKGYRMSPEPGCPGPVWVLMSSCWEARPPRPFKLAEKLA 470

Qy 480 RELRSGAGPASVSGDADGSTSPRSQ 505
 Db 471 ---SANWPWSWPGSYAVQVQPPSQ 492

RESULT 8
 US-09-741-154-4
 ; Sequence 4, Application US/09741154
 ; Patent No. 6437110
 ; GENERAL INFORMATION:
 ; APPLICANT: BEASLEY, Ellen M. et al
 ; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
 ; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
 ; TITLE OF INVENTION: THERAPE
 ; FILE REFERENCE: CL001061
 ; CURRENT APPLICATION NUMBER: US/09/741,154
 ; CURRENT FILING DATE: 2000-12-21
 ; NUMBER OF SEQ ID NOS: 4
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 4
 ; LENGTH: 386
 ; TYPE: PRT
 ; ORGANISM: Human
 ; US-09-741-154-4

Query Match Best Local Similarity 100.0%; Pred. No. 2.4e-163; DB 4; Length 386; Matches 386; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 122 WPHGKISQEAQVQLQPPEDGLFLVRESRARHPDGYVLCVSFGRDVTHYRVLHDHT 181
 Db 1 WPHGKISQEAQVQLQPPEDGLFLVRESRARHPDGYVLCVSFGRDVTHYRVLHDHT 60

Qy 182 EAVFCNLMDVNEHTSKDKGAICTKLRPKRKIGTKSAEELARAGMLNQHHTGA 241
 Db 61 EAVFCNLMDVNEHTSKDKGAICTKLRPKRKIGTKSAEELARAGMLNQHHTGA 121

Qy 242 GEGERGAVALQCEYLLGQKAVANIKCIVTAQAFDFTTAVTMTHOHENLVRLLGVLHQLY 301
 121 GEGERGAVALQCEYLLGQKAVANIKCIVTAQAFDFTTAVTMTHOHENLVRLLGVLHQLY 180

Db 302 IVMEVSKGNVNEFTRGRALVNTAQOLOFSIHYAEGMVELESKLVHRLAANNTLV 361
 Db 181 IVMEVSKGNVNEFTRGRALVNTAQOLOFSIHYAEGMVELESKLVHRLAANNTLV 240

Qy 362 EQLVAKVSDFGGLAKAERKGLDSSRLPVKWTAPRALKHKGFTSDWVSGDFTSPRSQEP 421
 Db 241 EQLVAKVSDFGGLAKAERKGLDSSRLPVKWTAPRALKHKGFTSDWVSGDFTSPRSQEP 300

Qy 422 RAPYPKMSLKEVSEAVEKGYRMSPEPGCPGPVWVLMSSCWEARPPRPFKLAEKLA 481
 301 RAPYPKMSLKEVSEAVEKGYRMSPEPGCPGPVWVLMSSCWEARPPRPFKLAEKLA 360

Qy 482 LRSAPASVSGDADGSTSPRSQEP 507
 Db 361 LRSAPASVSGDADGSTSPRSQEP 386

RESULT 9
US-09-741-154-2
Sequence 2, Application US/09741154
Patient No. 6437110
GENERAL INFORMATION:
APPLICANT: BEASLEY, Ellen M. et al
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC ACIDS, AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: C1001061
CURRENT APPLICATION NUMBER: US/09/741,154
CURRENT FILING DATE: 2000-12-21
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO: 2
LENGTH: 415
TYPE: PR^T
ORGANISM: Human
US-09-741-154-2

Query Match 75.3%; Score 2012; DB 4; Length 415;

Best Local Similarity 100.0%; Pred. No. 2.6e-163; Length 415;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 122 WFGKISGSEAVQQLQPPDGLVRESKRPQGDYVILCVSFGRDVHYVLHRDGLHTD 181
Db 30 WFGKISGSEAVQQLQPPDGLVRESKRPQGDYVILCVSFGRDVHYVLHRDGLHTD 89
Qy 182 EAVFCNLMDMEVTSKDKGAIKCKLVRKRRKHKTKSABELARAGWILNQHITLGQI 241
Db 90 EAEVFCNLMDMEVHSKDKGAIKCKLVRKRRKHKTKSABELARAGWILNQHITLGQI 149
Qy 242 GEGEFGAVI-QGEYJGQKVAVKNIKDVTAQAFDETAVMTKMOHENLYRLGVTIHLQIY 301
Db 150 GEGEFGAVI-QGEYJGQKVAVKNIKDVTAQAFDETAVMTKMOHENLYRLGVTIHLQIY 209
Qy 302 IVMERHVKSNLNVNLRTRGRALVNTAQLQFSHLVAEGMEYLESKKLYRD 361
Db 210 IVMERHVKSNLNVNLRTRGRALVNTAQLQFSHLVAEGMEYLESKKLYRD 269
Qy 362 EDLYAKVSDFGLAKAERKGKDSSLRPLVKVTAPEALKHGKFTSVDWVFGVLIWEVSYG 421
Db 270 EDLYAKVSDFGLAKAERKGKDSSLRPLVKVTAPEALKHGKFTSVDWVFGVLIWEVSYG 329
Qy 422 RAPVPMKSLKEVSEAVEKGYMRPEGGCPVHLMSSCWEAPRPPR 481
Db 330 RAPVPMKSLKEVSEAVEKGYMRPEGGCPVHLMSSCWEAPRPPR 389
Qy 482 LRSAGAPASVSGQDADGSTSPRSQEP 507
Db 390 LRSAGAPASVSGQDADGSTSPRSQEP 415

RESULT 10
US-08-604-989A-3
Sequence 3, Application US/08604989A
Patient No. 5834208
GENERAL INFORMATION:
APPLICANT: S.
TITLE OF INVENTION: NO. 58342081 Tyrosine Kinase
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
CURRENT APPLICATION DATA:

Query Match 47.5%; Score 1269; DB 2; Length 246;

Best Local Similarity 100.0%; Pred. No. 2.4e-100; Length 246;
Matches 246; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 233 QHLTIGAQIGEGFVGAVLQGEYJGQKVAVKNIKDVTAQAFDETAVMTKMOHENLYRL 292
Db 1 QHLTIGAQIGEGFVGAVLQGEYJGQKVAVKNIKDVTAQAFDETAVMTKMOHENLYRL 60
Qy 293 GVILHQGLYIVMERSKVLNLNVNLRTRGRALVNTAQLQFSHLVAEGMEYLESKKLYRD 352
Db 61 GVILHQGLYIVMERSKVLNLNVNLRTRGRALVNTAQLQFSHLVAEGMEYLESKKLYRD 120
Qy 353 LAARNILVSEDDLAKVSDFGLAKAERKGKDSSLRPLVKVTAPEALKHGKFTSVDWVFGV 412
Db 121 LAARNILVSEDDLAKVSDFGLAKAERKGKDSSLRPLVKVTAPEALKHGKFTSVDWVFGV 180
Qy 413 LLWEVFSYGRAPVPMKSLKEVSEAVEKGYMRPEGGCPVHLMSSCWEAPRPPR 472
Db 181 LLWEVFSYGRAPVPMKSLKEVSEAVEKGYMRPEGGCPVHLMSSCWEAPRPPR 240
Qy 473 KLAEKL 478
Db 241 KLAEKL 246

RESULT 11
US-08-426-509A-7
Sequence 7, Application US/08426509A
Patient No. 6320469
GENERAL INFORMATION:
APPLICANT: Ulrich, Axel
APPLICANT: Gishizky, Mikhail
APPLICANT: Sures, Iman G.
TITLE OF INVENTION: NOVEL MEGAKARYOCYTIC PROTEIN
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/426,509A
 FILING DATE: 21-APR-1995
 CLASSIFICATION: 435
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 08/232,545
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Coruzzi, Laura A.
 REGISTRATION NUMBER: 30,742
 REFERENCE/DOCKET NUMBER: 7683-0074-999
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212-90-9090
 TELEFAX: 212-869-9741
 TELEX: 66141 PENNIE
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 450 amino acids
 TYPE: amino acid
 STRANDEDNESS: unknown
 TOPOLOGY: unknown
 MOLECULE TYPE: NO. 6326469e
 US-08-426-509A-7

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Best Local Similarity 54.1%; Pred. No. 5.3e-98; Mismatches 115; Indels 3; Gaps 2; Matches 235; Conservative 81; Mismatches 115; Indels 3; Gaps 2;

Qy 47 WAPGTOCITKCENTRKPGEALFRKGDVVTLACEENKSWYRKHHTSGQEGLLAAGALR 106
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Qy 107 EREALSDAPKLSLMPWPHGKTSQEAQVQLOQPEDGLFLVRESARHPGDYVLCVSRGRDV 166
 Db 67 KREGVKGAKTSLMPWPHGKTRTREQAERLPPETGFLVKESTNPGDYLICVSCDGKV 126

Qy 167 IHYRVLRDGHITDRAVFCNLMDAVEHYSKDKGAICTKLYRKPKHGKTSQEAQVQLOQPEDGLFLVRESARHPGDYVLCVSRGRDV 166
 Db 127 EHYRIMHASKLISIDEVYFENLMDQVHYSIDAGLCTRLIKPKHGKTSQEAQVQLOQPEDGLFLVRESARHPGDYVLCVSRGRDV 186

Qy 227 GWLNLNQHHTLGAQIGEGERGAVIQLGEYLQGKVKVNNKICVTAQAFLEAVMTKQHE 286
 Db 187 GWALNKKELKLQQTIGKGEFGDMLGDYRKVNAVKCINKDADTAQFLAEASVMTQLRHS 246

Qy 287 NLVRLLGVILHQ-GLYTIVMEVSKGNLNUFLTRGRALVNTAQLOFSLVIAEGMEYLE 344
 Db 247 NLVQLQGIVIVEKGGIVIVTYPMAKSLVDSLRSRSVLGDCILKFSLDVCEAMEYLE 306

Qy 345 SKKLVHDLAARNLIVSEDLVAKVSKDGLAKERKGKGLDSSRLPVKWTAPPEALKHGFTSK 404
 Db 307 GNNFVHDLAARNLIVSEDLVAKVSKDGLKTREASSTDGTGLPVKWTAPPEALKHGFTSK 366

Qy 405 SDWWSFGVLLWEVFSYGRAPYKMSLKEVSEAVEKGYRMEPEGGCPGPVHLMSSWEAE 464
 Db 367 SDWWSFGVLLWEVFSYGRAPYKMSLKEVSEAVEKGYRMEPEGGCPGPVHLMSSWEAE 464

RESULT 12
 US 08-232-545-7
 Sequence 7, Application US/08232545
 ; Patent No. 6506578
 ; GENERAL INFORMATION:
 ; APPLICANT: Ulrich, Axel

APPLICANT: Gishizky, Mikhail
 APPLICANT: Sures, Iman G.
 TITLE OF INVENTION: No. 6506578el Megakaryocytic Protein Tyrosine
 NUMBER OF SEQUENCES: 21
 CORRESPONDENCE ADDRESS:
 ADDRESSEES: Pennie & Edmonds

STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: U.S.A.
 ZIP: 10036
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/732,545
 FILING DATE: 22-APR-1994
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Coruzzi, Laura A.
 REGISTRATION NUMBER: 30,742
 REFERENCE/DOCKET NUMBER: 7683-050
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212)869-9741
 TELEX: (212)869-9741
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 450 amino acids
 TYPE: amino acid
 STRANDEDNESS: unknown
 TOPOLOGY: unknown
 MOLECULE TYPE: protein
 US-08-232-545-7

Query Match 46.6%; Score 1245.5; DB 4; Length 450;
 Best Local Similarity 54.1%; Pred. No. 5.3e-98; Mismatches 115; Indels 3; Gaps 2; Matches 235; Conservative 81; Mismatches 115; Indels 3; Gaps 2;

Qy 47 WAPGTOCITKCENTRKPGEALFRKGDVVTLACEENKSWYRKHHTSGQEGLLAAGALR 106
 Db 8 WPSGTECIAKYNEHGTAEQDLPFCKGDVLTIVAVTKDPPNWYKAKNV-GREGIIPANYVQ 66

Qy 107 EREALSDAPKLSLMPWPHGKTSQEAQVQLOQPEDGLFLVRESARHPGDYVLCVSRGRDV 166
 Db 67 KREGVKGAKTSLMPWPHGKTRTREQAERLPPETGFLVKESTNPGDYLICVSCDGKV 126

Qy 167 IHYRVLRDGHITDRAVFCNLMDAVEHYSKDKGAICTKLYRKPKHGKTSQEAQVQLOQPEDGLFLVRESARHPGDYVLCVSRGRDV 166
 Db 127 EHYRIMHASKLISIDEVYFENLMDQVHYSIDAGLCTRLIKPKHGKTRTREQAERLPPETGFLVKESTNPGDYLICVSCDGKV 186

Qy 227 GWLNLNQHHTLGAQIGEGERGAVIQLGEYLQGKVKVNNKICVTAQAFLEAVMTKQHE 286
 Db 187 GWALNKKELKLQQTIGKGEFGDMLGDYRKVNAVKCINKDADTAQFLAEASVMTQLRHS 246

Qy 287 NLVRLLGVILHQ-GLYTIVMEVSKGNLNUFLTRGRALVNTAQLOFSLVIAEGMEYLE 344
 Db 247 NLVQLQGIVIVEKGGIVIVTYPMAKSLVDSLRSRSVLGDCILKFSLDVCEAMEYLE 306

Qy 345 SKKLVHDLAARNLIVSEDLVAKVSKDGLAKERKGKGLDSSRLPVKWTAPPEALKHGFTSK 404
 Db 307 GNNFVHDLAARNLIVSEDLVAKVSKDGLKTREASSTDGTGLPVKWTAPPEALKHGFTSK 366

Qy 405 SDWWSFGVLLWEVFSYGRAPYKMSLKEVSEAVEKGYRMEPEGGCPGPVHLMSSWEAE 464
 Db 367 SDWWSFGVLLWEVFSYGRAPYKMSLKEVSEAVEKGYRMEPEGGCPGPVHLMSSWEAE 464

RESULT 13
 PCT-US95-05008-7
 Sequence 7, Application PC/TUS9505008
 ; GENERAL INFORMATION:
 ; APPLICANT: Sugen, Inc.

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on:

July 29, 2003, 09:46:12 ;

Search time 44 Seconds
(without alignments)1828.963 Million cell updates/sec
US-09-977-261-2

Perfect score:

2671 MAGRSLSIVSNRRAFHG3CDSAE..... PASVSGQDADGSTSPRSQEP 507

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 1107863 seqs, 150726573 residuesTotal number of hits satisfying chosen parameters: 1107863
Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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ID AARY1133
ID AARY1133 standard; protein; 507 AA.

AC AARY1133:

DT 25-MAR-2003 (updated)

DT 27-OCT-1995 (first entry)

DE Cytoplasmic tyrosine kinase.

XX KW screening; tyrosine kinase; blood; cell differentiation;

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT Domain /note= "SH3 domain"

FT Domain /note= "SH2 domain"

FT Domain /note= "tyrosine kinase domain"

10 1245.5 46.6 450 21 AAY49418
11 1245.5 46.6 450 22 AAB84662
12 1245.5 46.6 450 22 AAG67444
13 1245.5 46.6 450 22 AAG67623
14 1245.5 46.6 450 24 ABR77428
15 979.5 36.7 820 22 ABR77215
16 916 34.3 357 23 AAU8677
17 753 28.2 502 23 AAE21689
18 745 27.9 567 23 AAG79573
19 742.5 27.8 508 21 AAB37700
20 736.5 27.6 509 21 AAY9420
21 735 27.5 533 14 AAB39705
22 733 27.4 533 21 AAY44447
23 733 27.4 533 22 AAB84661
24 733 27.4 533 21 AAY4451
25 727 27.2 533 21 AAY9420
26 727 27.2 536 14 ABR9706
27 727 27.2 536 23 ABB93339
28 727 27.2 536 23 AAB78678
29 727 27.2 536 24 ABB5260
30 724 27.1 1504 22 ABB60358
31 720.5 27.0 505 22 AAB9332
32 718 26.9 542 23 ABB93339
33 714 26.9 541 24 ABG7261
34 710 26.6 543 22 ABG10302
35 710 26.6 543 22 AAB84663
36 708 26.5 541 23 AAY4614
37 708 26.5 543 20 AAY24421
38 701.5 26.3 1130 24 ABG72620
39 699.5 26.2 565 22 ABG37778
40 699.5 26.2 1130 24 ABG72679
41 699.5 26.2 1130 24 ABG72689
42 698.5 26.2 1130 24 ABG72635
43 698.5 26.2 1130 24 ABG72643
44 698.5 26.2 1130 24 ABG72688
45 697.5 26.1 1130 24 ABG726210

PKA substrate, Csk

Amino acid sequenc

XX (ASAHI) ASAHI KASEI KOGYO KK.
 PA XX
 XX
 PT XX
 XX Sakano S;
 XX
 DR WPI; 1995-106842/74.
 DR N-PSDB; AAQ84888.
 PT Cytoplasmic tyrosine kinase and antibody recognising it - for screening chemical substances for tyrosine kinase inhibitory or activating activity for use as cancer therapy
 XX
 PS Claim 1; Page 42-44; 58pp; English.
 XX
 CC A cytoplasmic tyrosine kinase which has enhanced expression in connection with blood cell differentiation has been isolated from the human U9-7 blood cell line. The DNA sequences and antibodies raised against the enzyme, are useful for screening agents for inhibiting or activating activity on the tyrosine kinase, for use as anticancer agents.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 Sequence 507 AA:
 Query Match 100.0%; Score 2671; DB 16; Length 507;
 Best Local Similarity 100.0%; Pred. No. 8 6e-242; Mismatches 0; Indels 0; Gaps 0;
 PT Matches 507; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 QY 1 MAGRSLSVWRRAFGCDSAEELPRVSPRLRAHPPVSPARMTRWRPGTQCTKCHT 60
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 Db 61 RPKGELAERKGKVDTILACENKSWYRKHHTSGQEGILAGALRERREALSDAPKLSM 120
 CC 61 RPKGELAERKGKVDTILACENKSWYRKHHTSGQEGILAGALRERREALSDAPKLSM 120
 CC
 Db 121 PWFHGKISQEAQVQLQPEDGLEFLVRESRARHPDGYVLCVSGFGDVIHYRVLHDGHHTI 180
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 QY 181 DEAVFFCNLMDMVHYSKDKGAICTKLYVRPKRKGTKSAEELTARAGWLNQHHTLGQ 240
 CC 181 DEAVFFCNLMDMVHYSKDKGAICTKLYVRPKRKGTKSAEELTARAGWLNQHHTLGQ 240
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 CC
 QY 241 IGECEFGAVLQGEYLQGOKVAVKNKCDVTAQAFLEDETAVTMKHOHENLYRLLGVLHOGI 300
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 QY 301 YVMEHVSQGNLYNPLRGRALVNTAQDLOFSLHVAGMEYLESKKLVHDLARNILV 360
 CC 301 YVMEHVSQGNLYNPLRGRALVNTAQDLOFSLHVAGMEYLESKKLVHDLARNILV 360
 Db 361 SEDLVAKVSDFGGLAKAERKGKLDSSRLPVKWTAPALKKGKFTSKDSWVMSFGVLLWEFSY 420
 CC 361 SEDLVAKVSDFGGLAKAERKGKLDSSRLPVKWTAPALKKGKFTSKDSWVMSFGVLLWEFSY 420
 Db 361 SEDLVAKVSDFGGLAKAERKGKLDSSRLPVKWTAPALKKGKFTSKDSWVMSFGVLLWEFSY 420
 CC 421 GRAPYKMSLKEVSEAVKGYRMEPPEGCPGPVPHVLMSSCWEAPRPPFRKLAELKAR 480
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 QY 481 ELSAGAPASVSSDADGSTSPSQEP 507
 CC 481 ELSAGAPASVSSDADGSTSPSQEP 507
 CC
 RESULT 2
 AAQ15860
 ID AAQ15860 standard; Protein; 507 AA.
 XX
 AC XX
 XX
 DT 02-JAN-2003 (first entry)
 XX
 DE Human matk-related protein.

XX Human; allergic disease; matk gene; atopic dermatitis.
 KW XX
 OS XX
 Homo sapiens.
 PN XX
 WO200275304-A1.
 PD XX
 26-SEP-2002.
 PF XX
 01-MAR-2002; 2002WO-JP01916.
 XX
 PR XX
 21-MAR-2001; 2001JP-0081028.
 DR XX
 (GENO-) GENOX RES INC.
 PA (NIGE-) JAPAN GEN AGENCY NATION.
 XX
 Sugita Y, Heishi M, Kagaya S, Gunji S, Tsujimoto G;
 XX
 DR WPI; 2002-750572/81.
 DR N-PSDB; AAL50631.
 XX
 PT Examining allergic diseases by changes in expression level of matk gene in peripheral monocytes as indication, also applicable in screening compounds for treating allergic diseases e.g. atopic dermatitis.
 PT
 PS XX
 Disclosure; Page 52-55; 60pp; Japanese.
 PT
 QY 1 MAGRSLSVWRRAFGCDSAEELPRVSPRLRAHPPVSPARMTRWRPGTQCTKCHT 60
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 Db 61 RPKGELAERKGKVDTILACENKSWYRKHHTSGQEGILAGALRERREALSDAPKLSM 120
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 Db 121 PWFHGKISQEAQVQLQPEDGLEFLVRESRARHPDGYVLCVSGFGDVIHYRVLHDGHHTI 180
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 CC 181 DEAVFFCNLMDMVHYSKDKGAICTKLYVRPKRKGTKSAEELTARAGWLNQHHTLGQ 240
 Db 181 DEAVFFCNLMDMVHYSKDKGAICTKLYVRPKRKGTKSAEELTARAGWLNQHHTLGQ 240
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 QY 241 IGECEFGAVLQGEYLQGOKVAVKNKCDVTAQAFLEDETAVTMKHOHENLYRLLGVLHOGI 300
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 CC 301 YVMEHVSQGNLYNPLRGRALVNTAQDLOFSLHVAGMEYLESKKLVHDLARNILV 360
 Db 361 SEDLVAKVSDFGGLAKAERKGKLDSSRLPVKWTAPALKKGKFTSKDSWVMSFGVLLWEFSY 420
 CC 361 SEDLVAKVSDFGGLAKAERKGKLDSSRLPVKWTAPALKKGKFTSKDSWVMSFGVLLWEFSY 420
 QY 421 GRAPYKMSLKEVSEAVKGYRMEPPEGCPGPVPHVLMSSCWEAPRPPFRKLAELKAR 480
 CC 421 GRAPYKMSLKEVSEAVKGYRMEPPEGCPGPVPHVLMSSCWEAPRPPFRKLAELKAR 480
 Db 421 GRAPYKMSLKEVSEAVKGYRMEPPEGCPGPVPHVLMSSCWEAPRPPFRKLAELKAR 480

QY 481 ELRSAGAPASVSGQDADGSTSPRSQEP 507
 ID AAR84181 standard; Protein; 507 AA.
 Db 481 ELRSAGAPASVSGQDADGSTSPRSQEP 507

RESULT 3

XX AAR84181
 ID AAR84181 standard; Protein; 507 AA.
 AC AAR84181;
 XX 26-MAR-1996 (first entry)

XX DE . Megakaryocyte kinase MKK1.
 DE . Megakaryocyte kinase MKK1.
 XX KW Megakaryocyte kinase-1; MKK1; cytoplasmic tyrosine kinase;
 cellular signal transduction; leukaemia; thrombocytopenia.
 XX OS Homo sapiens.

XX Key Location/Qualifiers
 FT Domain 48..111 /label= SH3_domain
 FT Domain 122..196 /label= SH2_domain
 FT Domain 233..478 /label= Catalytic_domain

XX PN W09529185-A1.
 PD 02-NOV-1995.
 XX PP 24-APR-1995; 95WO-US05008.
 PR 21-APR-1995; 95US-0426509.
 PR 22-APR-1994; 94US-023245.
 XX PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
 XX PA (SUGE-) SUGEN INC.
 PT Gishizky M, Sures I, Ullrich A;
 XX DR WPI; 1995-382959/49.
 DR N-PSDB; AAT00616.

XX PT New polypeptide(s) encoding megakaryocyte tyrosine kinase(s) - used to develop probes for the treatment and diagnosis of kinase related signal transduction abnormalities.

XX PS Claim 15; Fig 1A-C; 82pp; English.

XX CC Human megakaryocyte kinase MKK1 (AAR84181) is a 58 kDa cytosolic tyrosine kinase showing 54% homology with csk. It appears to play a regulatory role in the growth and differentiation of megakaryocytes and perhaps neural tissues. Recombinant MKK1 can be produced in host cells by expression of encoding cDNA (AAT00616), and used in the treatment and diagnosis of e.g. leukaemia and thrombocytopenia.

XX SQ Sequence 507 AA;

Query Match 99.9%; Score 2668; DB 16; Length 507;
 Best Local Similarity 99.8%; Pred. No. 1..6e-241;
 Matches 506; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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 Db 61 RPKGELAFRKDQVYTLAECKNSWYKHTSGGEGGLAAGALREREAISADPKLSLM 120
 Qy 61 RPKGELAFRKDQVYTLAECKNSWYKHTSGGEGGLAAGALREREAISADPKLSLM 120

Db 301 YTMVHYSKGNLVNFRLTRGRALVNTAOLQTSLLVAGMELTESKKVHROIAARNLIV 360
 301 YTMVHYSKGNLVNFRLTRGRALVNTAOLQTSLLVAGMELTESKKVHROIAARNLIV 360
 361 SEDLVAKYVSDFGLAKAERKGLOSLRPLVKWTAAPEALKHGKFPSKSDWSFGYLWEVFSY 420
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 QY 421 GRAYPKMSLKEVESEAVERGYRMEPPGCPGPVPHVLMSCWEAPRPPRPERKLAELAR 480
 Db 421 GRAYPKMSLKEVESEAVERGYRMEPPGCPGPVPHVLMSCWEAPRPPRPERKLAELAR 480
 QY 481 ELRSAGAPASVSGQDADGSTSPRSQEP 507
 Db 481 ELRSAGAPASVSGQDADGSTSPRSQEP 507

RESULT 4

XX AAR71132
 ID AAR71132 standard; Protein; 466 AA.
 AC AAR71132;
 XX DT 25-MAR-2003 (updated)
 DT 27-OCT-1995 (first entry)

XX DE N-terminal truncated cytoplasmic tyrosine kinase.

XX KW cytoplasmic; tyrosine kinase; blood; cell differentiation; screening; anticancer agent; SH3; src homology domain.

XX OS Homo sapiens.

XX Key Location/Qualifiers
 FT Domain 7..70 /note= "SH3 domain"
 FT Domain 81..155 /note= "SH2 domain"
 FT Domain 192..438 /note= "tyrosine kinase domain"

XX PN W09506113-A1.
 PD 02-MAR-1995.
 XX PR 25-AUG-1994; 94WO-JP01411.
 XX PR 25-AUG-1993; 93JP-0210403.
 PR 29-MAR-1994; 94JP-0058553.
 XX PA (ASAH) ASAHI KASEI KOGYO KK.
 PI Sakano S;
 XX DR WPI; 1995-106842/14.
 DR N-PSDB; AAO84888.

XX PT Cytoplasmic tyrosine kinase and antibody recognising it - for screening chemical substances for tyrosine kinase inhibitory or activating activity for use as cancer therapy
 XX

XX	Claim 1; Page 40-42; 58pp; English.
CC	A cytoplasmic tyrosine kinase which has enhanced expression in connection with blood cell differentiation has been isolated from the human UT-7 blood cell line. This sequence comprises an N-terminal truncated fragment of the enzyme (residues 42-507 of HAT71131). The DNA sequences and antibodies raised against the enzyme, are useful for screening agents for inhibiting or activating activity on the tyrosine kinase, for use as anticancer agents. (Updated on 25 MAR-2003 to correct PN field.)
CC	CC
CC	CC
CC	CC
XX	Sequence 466 AA;
Query Match	91.5%; Score 2444; DB 16; Length 466;
Best Local Similarity	100.0%; Pred. No. 1.6e-220;
Matches	466; Conservative 0; Mismatches 0;
Indels	0; Gaps 0;
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Qy	61 AGALREREALSAADPKLSSLMMWFGHTSGQEAQVQIOPPEGLFLVRESARHPGDXVLCVS 120
Db	162 FGDRDHYRLHRDQHDLTDEAVFCNLMDWVHYSKDKGAICTKLVRPKRKHGKSAE 221
Qy	121 FGDRDHYRLHRDQHDLTDEAVFCNLMDWVHYSKDKGAICTKLVRPKRKHGKSAE 180
Db	222 ELARGWGLMLQHLLTGAQIGEGERGEAVLQGEYLGQKAVKNIKDVTAQAFDLDPTAVMT 281
Qy	181 ELARGWGLMLQHLLTGAQIGEGERGEAVLQGEYLGQKAVKNIKDVTAQAFDLDPTAVMT 240
Db	282 KMHQHENLVLRLGVLHQHGLYTMENIVSKGNLNUFTRTRGRALVNTQOLQFLSHAEQME 341
Qy	241 KMHQHENLVLRLGVLHQHGLYTMENIVSKGNLNUFTRTRGRALVNTQOLQFLSHAEQME 300
Db	342 YLESKRLVHDLAARNILVSDLWAKVSDGLAKERKGDDSSRPLPKWTAPEAKRHKGF 401
Qy	301 YLESKRLVHDLAARNILVSDLWAKVSDGLAKERKGDDSSRPLPKWTAPEAKRHKGF 360
Db	402 TSKSWYSFWCVLWVWFSYGRAPYKMSLKEVSEVEKGYRMEPEPGECPGPVPHVLMSSCW 461
Qy	361 TSKSWYSFWCVLWVWFSYGRAPYKMSLKEVSEVEKGYRMEPEPGECPGPVPHVLMSSCW 420
Db	462 EAEPARRPPEPKLAKLAKLARELRSAGAPASVSGQDADGSTSPRSQEP 507
Qy	421 EAEPARRPPEPKLAKLAKLARELRSAGAPASVSGQDADGSTSPRSQEP 466
RESULT 5	
AAW64454	
ID	AAW64454 standard; Protein; 528 AA.
XX	
AC	AAW64454;
XX	
DT	16-OCT-1998 (first entry)
DE	Human matK protein.
XX	
Breast; cancer; matK; CSK homologous kinase; CHK; detection; diagnosis; KW cyctoplasmic protein; tyrosine kinase; Erbb-2; negative regulator; XX mitogenic signalling.	
OS	Homo sapiens.
PN	W0983074-A1.
XX	
PD	16-JUL-1998.
XX	
PF	07-JAN-1998; 98WO-US00420.
PR	16-JUN-1997; 97US-0816882.
XX	
Query Match	91.1%; Score 2434.5; DB 19; Length 528;
Best Local Similarity	93.3%; Pred. No. 1.5e-219;
Matches	472; Conservative 1; Mismatches 18;
Indels	15; Gaps 3;
Db	1 MAGRSGLSVWNRWFGCDAEELPRVSEPRFLRWRHPPVPSAAMPTRWAPGTCITCCEHT 60
Qy	1 MAGRSGLSVWNRWFGCDAEELPRVSEPRFLRWRHPPVPSAAMPTRWAPGTCITCCEHT 60
Db	61 RPKPGELAERKGDDWVITLEACENSKWYRKHTSGEGLLAAGALREREALSAADPKLSL 119
Qy	61 RPKPGELAERKGDDWVITLEACENSKWYRKHTSGEGLLAAGALREREALSAADPKLSL 120
Db	120 MPWFHGKISGQEAQVQIOPPEGLFLVRESARHPGDXVLCVSFGDGRVHYRLHRDQHLT 179
Qy	121 MPWFHGKISGQEAQVQIOPPEGLFLVRESARHPGDXVLCVSFGDGRVHYRLHRDQHLT 180
Db	180 IDEAVFCNLMDWVHYSKDKGAICTKLVRPKRKHGKTSABELARGLWLNQHLLTGA 239
Qy	181 IDEAVFCNLMDWVHYSKDKGAICTKLVRPKRKHGKTSABELARGLWLNQHLLTGA 240
Db	240 QIGEGEFGAVQVQGEYLGQKAVKNIKDVTAQAFDFTAVMTKMQHENLVLRLGVLHOG 299
Qy	241 QIGEGEFGAVQVQGEYLGQKAVKNIKDVTAQAFDFTAVMTKMQHENLVLRLGVLHOG 300
Db	300 LYIVMHRVSKGNLNUFTRTRGRALVNTQOLQFLSHAEQMEYLELESKKLVRDLAARNIL 359
Qy	301 LYIVMHRVSKGNLNUFTRTRGRALVNTQOLQFLSHAEQMEYLELESKKLVRDLAARNIL 360
Db	360 VSEDLWAKVSKGNLNUFTRTRGRALVNTQOLQFLSHAEQMEYLELESKKLVRDLAARNIL 360
Qy	361 VSEDLWAKVSKGNLNUFTRTRGRALVNTQOLQFLSHAEQMEYLELESKKLVRDLAARNIL 361
Db	420 YGRAPYKMSLKEVSEVEKGYRMEPEPGECPGPVPHVLMSSCWAEAPRPPRKLAKLA 479
Qy	420 YGRAPYKMSLKEVSEVEKGYRMEPEPGECPGPVPHVLMSSCWAEAPRPPRKLAKLA 479
Db	480 KLRSLRAGAPASVSGQDADGSTSPRSQ 505
Qy	480 KLRSLRAGAPASVSGQDADGSTSPRSQ 505
PR	08-JAN-1997; 97US-0035228.
XX	
PA	(BETH-) BETH ISRAEL DEACONESS MEDICAL CNT.
XX	
PT	Avraham H, Groopman JE;
XX	
DR	N-PSDB; AA944497.
XX	
PT	Detecting breast cancer by detecting Csk homologous kinase expression - especially in humans and use of Csk homologous kinase in treatment or prophylaxis of breast cancer and for producing medicaments
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PS	Disclosure; Fig 2; 54pp; English.
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Qy	1 MAGRSGLSVWNRWFGCDAEELPRVSEPRFLRWRHPPVPSAAMPTRWAPGTCITCCEHT 60
Db	61 RPKPGELAERKGDDWVITLEACENSKWYRKHTSGEGLLAAGALREREALSAADPKLSL 119
Qy	61 RPKPGELAERKGDDWVITLEACENSKWYRKHTSGEGLLAAGALREREALSAADPKLSL 120
Db	120 MPWFHGKISGQEAQVQIOPPEGLFLVRESARHPGDXVLCVSFGDGRVHYRLHRDQHLT 179
Qy	121 MPWFHGKISGQEAQVQIOPPEGLFLVRESARHPGDXVLCVSFGDGRVHYRLHRDQHLT 180
Db	180 IDEAVFCNLMDWVHYSKDKGAICTKLVRPKRKHGKTSABELARGLWLNQHLLTGA 239
Qy	181 IDEAVFCNLMDWVHYSKDKGAICTKLVRPKRKHGKTSABELARGLWLNQHLLTGA 240
Db	240 QIGEGEFGAVQVQGEYLGQKAVKNIKDVTAQAFDFTAVMTKMQHENLVLRLGVLHOG 299
Qy	241 QIGEGEFGAVQVQGEYLGQKAVKNIKDVTAQAFDFTAVMTKMQHENLVLRLGVLHOG 300
Db	300 LYIVMHRVSKGNLNUFTRTRGRALVNTQOLQFLSHAEQMEYLELESKKLVRDLAARNIL 359
Qy	301 LYIVMHRVSKGNLNUFTRTRGRALVNTQOLQFLSHAEQMEYLELESKKLVRDLAARNIL 360
Db	360 VSEDLWAKVSKGNLNUFTRTRGRALVNTQOLQFLSHAEQMEYLELESKKLVRDLAARNIL 360
Qy	361 VSEDLWAKVSKGNLNUFTRTRGRALVNTQOLQFLSHAEQMEYLELESKKLVRDLAARNIL 361
Db	420 YGRAPYKMSLKEVSEVEKGYRMEPEPGECPGPVPHVLMSSCWAEAPRPPRKLAKLA 479
Qy	420 YGRAPYKMSLKEVSEVEKGYRMEPEPGECPGPVPHVLMSSCWAEAPRPPRKLAKLA 479
Db	480 KLRSLRAGAPASVSGQDADGSTSPRSQ 505
Qy	480 KLRSLRAGAPASVSGQDADGSTSPRSQ 505
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Db	61 RPKPGELAERKGDDWVITLEACENSKWYRKHTSGEGLLAAGALREREALSAADPKLSL 119
Qy	61 RPKPGELAERKGDDWVITLEACENSKWYRKHTSGEGLLAAGALREREALSAADPKLSL 120
Db	120 MPWFHGKISGQEAQVQIOPPEGLFLVRESARHPGDXVLCVSFGDGRVHYRLHRDQHLT 179
Qy	121 MPWFHGKISGQEAQVQIOPPEGLFLVRESARHPGDXVLCVSFGDGRVHYRLHRDQHLT 180
Db	180 IDEAVFCNLMDWVHYSKDKGAICTKLVRPKRKHGKTSABELARGLWLNQHLLTGA 239
Qy	181 IDEAVFCNLMDWVHYSKDKGAICTKLVRPKRKHGKTSABELARGLWLNQHLLTGA 240
Db	240 QIGEGEFGAVQVQGEYLGQKAVKNIKDVTAQAFDFTAVMTKMQHENLVLRLGVLHOG 299
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Db	300 LYIVMHRVSKGNLNUFTRTRGRALVNTQOLQFLSHAEQMEYLELESKKLVRDLAARNIL 359
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Db	420 YGRAPYKMSLKEVSEVEKGYRMEPEPGECPGPVPHVLMSSCWAEAPRPPRKLAKLA 479
Qy	420 YGRAPYKMSLKEVSEVEKGYRMEPEPGECPGPVPHVLMSSCWAEAPRPPRKLAKLA 479
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PR	08-JAN-1997; 97US-0035228.
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Qy	181 IDEAVFCNLMDWVHYSKDKGAICTKLVRPKRKHGKTSABELARGLWLNQHLLTGA 240
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Db	300 LYIVMHRVSKGNLNUFTRTRGRALVNTQOLQFLSHAEQMEYLELESKKLVRDLAARNIL 359
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Db	420 YGRAPYKMSLKEVSEVEKGYRMEPEPGECPGPVPHVLMSSCWAEAPRPPRKLAKLA 479
Qy	420 YGRAPYKMSLKEVSEVEKGYRMEPEPGECPGPVPHVLMSSCWAEAPRPPRKLAKLA 479
Db	480 KLRSLRAGAPASVSGQDADGSTSPRSQ 505
Qy	480 KLRSLRAGAPASVSGQDADGSTSPRSQ 505
PR	08-JAN-1997; 97US-0035228.
XX	
PA	(BETH-) BETH ISRAEL DEACONESS MEDICAL CNT.
XX	
PT	Avraham H, Groopman JE;
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Db	61 RPKPGELAERKGDDWVITLEACENSKWYRKHTSGEGLLAAGALREREALSAADPKLSL 119
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Db	180 IDEAVFCNLMDWVHYSKDKGAICTKLVRPKRKHGKTSABELARGLWLNQHLLTGA 239
Qy	181 IDEAVFCNLMDWVHYSKDKGAICTKLVRPKRKHGKTSABELARGLWLNQHLLTGA 240
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PR	08-JAN-1997; 97US-0035228.
XX	
PA	(BETH-) BETH ISRAEL DEACONESS MEDICAL CNT.
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Qy	1 MAGRSGLSVWNRWFGCDAEELPRVSEPRFLRWRHPPVPSAAMPTRWAPGTCITCCEHT 60

Db	471	---	SANWPRSPGSPYAVQVPPSQ	492	Qy	302	TYMEHVSKGNLVNFRLTRGRALVNTAQOLQFSIHLVAGMEYLESKKKLVHDLAARNLVS	361
RESULT 6					Db	210	TYMEHVSKGNLVNFRLTRGRALVNTAQOLQFSIHLVAGMEYLESKKKLVHDLAARNLVS	269
AAU9575	ID	AAU9575	standard; Protein; 415 AA.		Qy	362	EDIVAKISDFGLAKAERKGKGLSSRLPKWTAELAKGKFSKSDWSFGVILWESYIG	421
XX	AC	AAU9575;			Db	270	EDIVAKISDFGLAKAERKGKGLSSRLPKWTAELAKGKFTSKSDWSFGVILWESYIG	329
XX	DT	21-OCT-2002	(first entry)		Qy	422	RAPYPKASLKEYSEAVENGYRMEPECGCPGPVHVLMSCWAEPPRPPFRKLAKLARE	481
XX	DE	Human kinase related to tyrosine kinase family.			Db	330	RAPYPKASLKEYSEAVENGYRMEPECGCPGPVHVLMSCWAEPPRPPFRKLAKLARE	389
XX	KW	Human; kinase; tyrosine kinase; kinase mediated disorder; hematopoietic disorder; cell signal transduction disorder; cancer; haemostatic; cytostatic; enzyme.			Qy	482	LRSAGAPASVSGQDAGSTSRSQEP	507
XX	OS	Homo sapiens.			Db	390	LRSAGAPASVSGQDAGSTSRSQEP	415
XX	PN	W0200252018-A2.			RESULT 7			
XX	PD	04-JUL-2002.			AAR71131			
XX	PF	19-DEC-2001; 2001WO-US48546.			ID	AAR71131	standard; Protein; 246 AA.	
XX	PR	21-DEC-2000; 2000US-0741154.			XX	AA	AAR71131;	
XX	PA	(PEKE) PE CORP NY.			XX	XX		
XX	PI	Beasley EM, Shao W, Ketchum K, Di Francesco V;			DT	25-MAR-2003	(updated)	
XX	PT	WPI; 2002-583568/62.			DT	27-OCT-1995	(first entry)	
DR	DR	DR-N-PSDB; ABR88791; ABR88792.			XX	DE	Tyrosine kinase domain of cytoplasmic tyrosine kinase.	
XX	PS	New isolated human kinase proteins and genes, useful in developing drugs, as well as for diagnosing, preventing or treating disorders associated with defective cell signal transduction, e.g. cancer or haematopoietic disorders -			XX	KW	cytoplasmic; tyrosine kinase; blood; cell differentiation; screening; anticancer agent.	
XX	CC	The present invention relates to the isolation of a novel human kinase related to the tyrosine kinase family, and polynucleotide sequences encoding it. The gene encoding the kinase of the invention maps to chromosome 19. The kinase may be used for identifying a modulator of the kinase, an agent that binds to the kinase, or for identifying other members of the family. The kinase may also be used to raise antibodies which may be used in immunoassays or drug screening assays. The sequences of the invention may be used for treating a disease or condition mediated by a human kinase such as haematopoietic disorders and other disorders associated with defective cell signal transduction (e.g. cancer). The polynucleotide sequences encoding the kinase are useful for isolating and purifying the kinase, and as probes or primers. The present sequence represents the human kinase of the invention.			XX	OS	Homo sapiens.	
XX	CC	Claim 1; FIG 2A; 78PP; English.			XX	PN	W09506113-A1.	
XX	CC	PR	02-MAR-1995.		XX	PD	02-MAR-1995.	
XX	CC	PR	25-AUG-1994; 94WO-JP01411.		XX	PP	25-AUG-1994; 94WO-JP01411.	
XX	CC	PR	25-AUG-1993; 93JP-0210403.		XX	PR	25-AUG-1993; 93JP-0210403.	
XX	CC	PR	29-MAR-1994; 94JP-0058553.		XX	PR	29-MAR-1994; 94JP-0058553.	
XX	CC	PR	29-MAR-1994; 94JP-0058553.		XX	PA	(ASAHI) ASAHI KASEI KOGYO KK.	
XX	CC	PR	29-MAR-1994; 94JP-0058553.		XX	PI	Sakano S;	
XX	CC	PR	29-MAR-1994; 94JP-0058553.		XX	DR	WPI; 1995-106842/14.	
XX	CC	PR	29-MAR-1994; 94JP-0058553.		XX	DR	DR-N-PSDB; AAO84888.	
XX	CC	PS	Claim 1; Page 39; 58pp; English.		XX	CC	A cytoplasmic tyrosine kinase which has enhanced expression in connection with blood cell differentiation has been isolated from the human utr-7 blood cell line. This sequence comprises the tyrosine kinase domain of the enzyme (residues 192-470 of AAR71132; residues 233-478 of AAR71133). The DNA sequences and antibodies raised against the enzyme, are useful for screening agents for inhibiting or activating activity on the tyrosine kinase, for use as anticancer agents. (Updated on 25-MAR-2003 to correct PN field.)	
XX	CC	PS	Claim 1; Page 39; 58pp; English.		XX	CC	A cytoplasmic tyrosine kinase which has enhanced expression in connection with blood cell differentiation has been isolated from the human utr-7 blood cell line. This sequence comprises the tyrosine kinase domain of the enzyme (residues 192-470 of AAR71132; residues 233-478 of AAR71133). The DNA sequences and antibodies raised against the enzyme, are useful for screening agents for inhibiting or activating activity on the tyrosine kinase, for use as anticancer agents. (Updated on 25-MAR-2003 to correct PN field.)	
Qy	182	EAFFCNLMDMTHYSKDKGATCTKLYPRKRKHGTSAEELARAGLILNQQLHTIGAQI	241	Qy	303	QHLTIGAQIGESEFGAVLQGEYLQKAVKNIKCDVTAQAFDETAVMTKMOHENLVRLLGVILHOGLY	292	
Db	90	EAFFCNLMDMTHYSKDKGATCTKLYPRKRKHGTSAEELARAGLILNQQLHTIGAQI	149	Qy	233	QHLTIGAQIGESEFGAVLQGEYLQKAVKNIKCDVTAQAFDETAVMTKMOHENLVRLLGVILHOGLY	209	
Db	30	WFRGKTLSSQEAQVQOLQPEDGLFLVRESARHPGDYVLCVSFGRDVHVRLLGVILHOGLY	89	Qy				

Db	1	QHLTGGAQIGEGERGAVLQGEYLGOKVAKNIKCDVQAFDLEPAVMTKMOHENLVRRL 60	SQ	Sequence	459 AA;
Qy	293	GVLHOGGLYIYMEHYSKGNIYVFLRURGRALVNTQALQFLSFLHVAEGMELLESKVLVRD 352	Query Match	46.7%	Score 1247.5; DB 22; Length 459;
Db	61	GVLHOGGLYIYMEHYSKGNIYVFLRURGRALVNTQALQFLSFLHVAEGMELLESKVLVRD 120	Best Local Similarity	53.2%	Pred No. 3.7e-108;
Db	353	LAARNITLVSRLVAKVSDGLAKAERKGGLDSSRLPVKWTPEALKHGKFTSKDQWNSFGV 412	Matches	238;	Conservative 82; Mismatches 118; Indels 9; Gaps 3;
Qy	121	LAARNITLVSRLVAKVSDGLAKAERKGGLDSSRLPVKWTPEALKHGKFTSKDQWNSFGV 180	Qy	40	ARMPTR----RMAPGQTCITKEHTRKPGELAFRKGDYVTLIEAGENKSMYRKHHT 93
Db	413	LLWEFSYGRAPYKPKMSLKEVSEAVEKGMRMEPPBCCPGIVHVLMSSCWEEAPARRPPR 472	Db	4	ARAPPKMSAQAAWNPSGTCIAYKVNPHGTAEQDLFCKGDVLTAVTPDNWYKAKVY 63
Qy	181	LLWEFSYGRAPYKPKMSLKEVSEAVEKGMRMEPPBCCPGIVHVLMSSCWEEAPARRPPR 240	Qy	94	SGQEGLLAAGALREFEALSDPKSLMPWPHGKTSQGEAVQOLQPPEDGLFLYRESARHP 153
Qy	473	KLAEKL 478	Db	64	-GRECIIIPANYQVQREGVAKTGSKLMPPFHGKTSQGEAVQOLQPPEDGLFLYRESARHP 122
Db	241	KLAEKL 246	Db	123	GDYTCIVSCDGKVEHYRIMHASKLISIDEVIFENLMOVLEHTSDADGLCTRLKPKW 182
RESULT 8			Qy	214	HGTKSAAEELARASWLLNIOHLTGGAQIGEGERGAVLQGEYLGOKVAKNIKCDVQAF 273
AA013873			Db	183	EGTVAQDEFYRSGWALNHLKELKLQTICKGEFQDVMGDRYGNKVAVKCIKDATACF 242
ID	AA013873	standard; Protein; 459 AA.	XX	274	LDEAVMTKMOHENLVRLLGVLHQ--GLIYIYMEHYSKGNIYVFLRURGRALVNTQALQ 331
AC	AA013873;		Db	243	LAEASVMTQURHSNLVQLLGIVVEREKGGLYIYTEMYMAKSLVYDYLRSRGRSVLGDCLLK 302
XX			Qy	332	FSLRHVAEGMELLESKVLVRDHLAARNILVYEDLVAKVSDFGLAKAERKGGLDSSRLPVKWT 391
DE			Db	303	FSLDVCEAMEYLEGINFVHDLAARNLYSEDNTVAKVSDFGLIKEASSTQDPIGKLPVKT 362
KW			Qy	392	APPEALKHGKETSKSWSWGSVLLMVFBSYGRAPYKPKMSLKEVSEAVEKGMRMEPPBCCPG 451
KW			Db	363	APEARREKFKTSQWNSFGVLLMVFBSYGRAPYKPKMSLKEVSEAVEKGMRMEPPBCCPG 422
KW			Qy	452	PVRYMVSWEAERRRPFPKLAEKL 478
OS			Db	423	AVYEVNKNCHLDAMRPSFLQRLQD 449
XX			XX		
PN	W0200164835-A2.		XX		
PD	07-SEP-2001.		XX		
XX			XX		
PF	26-FEB-2001; 2001WO-US04927.		XX		
XX			XX		
PR	28-FEB-2000; 2000US-0515126.		AC		
PR	18-MAY-2000; 2000US-0577409.		XX		
XX			AY44448;		
PA	(HYSE-) HYSEQ INC.		XX		
XX			DT		
PT	Tang YT, Liu C, Drmanac RT;		22-MAR-2000 (first entry)		
XX			XX		
DR	WPI; 2001-514838/56.		DE		
DR	N-PSDB; AA193804.		Wild-type human c-Src tyrosine kinase.		
XX			XX		
PT	Isolated nucleic acids and polypeptides, useful for preventing		Angiogenesis; tyrosine kinase; Src; inhibition; activation; modulate;		
PT	diagnosing and treating e.g. leukaemia, inflammation and immune		human; viral expression vector; replication competent; mutant Src;		
PT	disorders.		inflammatory disease; arthritis; rheumatoid arthritis; restenosis;		
XX			KW		
PS	Claim 20; SEQ ID NO 27765; 1399pp + Sequence Listing; English.		diabetic retinopathy; osteoporosis; cancer.		
XX			XX		
CC	The invention relates to human polynucleotides (AAI7941-AAI93841) and		Homo sapiens.		
CC	the encoded proteins (AA001010-AA013910) that exhibit activity elating to		OS		
CC	cytokine, cell proliferation or cell differentiation or which may induce		XX		
CC	production of other cytokines in other cell populations. The		PN		
CC	polynucleotides and polypeptides are useful in gene therapy, vaccines or		W0951590-A1.		
CC	peptide therapy. The polypeptides have various cytokine-like activities,		XX		
CC	e.g. stem cell growth factor activity, haematopoiesis regulating		PD		
CC	activity, tissue growth factor activity, immunomodulatory activity and		02-DEC-1999.		
CC	activity/inhibit activity and may be useful in the diagnosis and/or		XX		
CC	treatment of cancer, leukaemia, nervous system disorders, arthritis and		28-MAY-1999;		
CC	inflammation.		99WO-US11780.		
CC	Note: The sequence data for this patent did not form part of the printed		PR		
CC	specification, but was obtained in electronic format directly from WIPO		29-MAY-1998;		
XX	at ftp.wipo.int/pub/published_pct_sequences.		98US-0087220.		
XX			XX		
PT	Using tyrosine kinase Src for modulating angiogenesis in tissues useful		(SCRI) SCRIPPS RES INST.		
PT	in, e.g. treatment of chronic articular rheumatism -		XX		
PT	WPI; 2000-116335/10.		Cheresh DA, Elceirri B, Schwartzberg PL;		
PT	N-PSDB; AA229701.		XX		

RESULT 11

Db AAB84662

QY ID AAB84662 standard; Protein; 450 AA.

XX

XX AC AAB84662;

XX DT 05-SEP-2001 (first entry)

DE Amino acid sequence of human tyrosine kinase protein Src.

XX

KW Vascular permeability; tyrosine kinase protein; Src; Yes; stroke; myocardial infarction; restenosis; trauma; blood vessel; atherosclerosis; diabetic retinopathy; inflammatory disease; infection; arthritis; adult respiratory distress syndrome; ARDS; rheumatoid arthritis; diabetic retinopathy; psoriasis; neovascular glaucoma; capillary proliferation; osteoporosis; cancer.

XX OS Homo sapiens.

XX WO200145751-A1.

PR 29-MAR-2000; 2000US-0538248.

PD 28-JUN-2001.

XX PF 22-DEC-2000; 2000WO-US35396.

XX PR 22-DEC-1999; 99US-0470881.

PR 29-MAR-2000; 2000US-0538248.

XX PA (SCR) SCRIPPS RBS INST.

XX PT Chereesh DA, Elceirri B, Paul R;

XX DR WPI; 2001-417982/44.

XX N-PSDB; AAH28358.

XX PT Modulating vascular permeability in tissues, including inflamed tissue, tissues associated with stroke, myocardial infarction, by contacting the tissue with tyrosine kinase protein Src, Yes or their modified forms -

XX PS Disclosure; Fig 4; 133pp; English.

XX The specification describes a method for modulating vascular permeability in a tissue suffering from a disease condition. The method comprises contacting the tissue with a pharmaceutical composition comprising tyrosine kinase protein Src, Yes or their mixtures or nucleic acid expressing them. The method is useful for modulating vascular permeability in tissues, including inflamed tissue, tissues associated with stroke, myocardial infarction or other blockage of normal flow, tissues undergoing restenosis, psoriatic, retinal tissue and similar tissues. Pathologies which may be treated include include trauma to blood vessels, and other systemic pathological events such as atherosclerosis, diabetic retinopathy, inflammatory disease due to infection by microbial agents and arthritis. Other diseases which can be treated include adult respiratory distress syndrome (ARDS), rheumatoid arthritis, diabetic retinopathy, psoriasis, neovascular glaucoma, capillary proliferation in atherosclerotic plaques and osteoporosis and cancer associated disorders such as solid tumours, solid tumour metastases, angiofibromas and hemangiomas. The present sequence represents human Src, and is used in the method of the invention.

XX Sequence 450 AA.

XX

Query Match 46.6%; Score 1245.5; DB 22; Length 450; Best Local Similarity 54.1%; Pred. No. 5.5e-108; Matches 235; Conservative 81; Mismatches 115; Indels 3; Gaps 2;

QY 47 WARPQCTKCEHTRPKPGELAFRKGDYVTLFACENKSWYRKHHTSGQEGGLAAGALR 106

8 WPSGTECIAKYNFHFGTAECQDLPPCKGKDYLITIVAVTKDPNWYKAKNVK-GREGILIPANYVQ 66

QY 107 EREALSAPKKLSLMPWFKGKISQEAQVQQLQPEDGFLWRESARHRCGDDVLCVSGFGRDV 166

Db 67 KRIGVKAGTKLSLMPWPHGKITREQABRLYPPETGFLVRSTNPQGDYLVCSDGKV 126

QY 167 IHRVVLHRDHGHTIDEAVFFCNUMLDMEHYSKDKGAICTKLVRPKRKGHTKSAEELARA 226

XX 127 EHRIMYHASKLISIDEEVYENLQMVLYEHTSDADGLCTRLKPKVMEGTVAQDFYRS 186

Db 227 GWLNLQHILTGQIGGEGFAGVQGLQYGLQKAVAKNQKCVTAOFPLDEPAVMTMHE 286

Db 187 GWALNMBKLLOLTIGKCEFGDVMGDYGRNKVAVKCIKNDATAQAFLAESVMTQURHS 246

QY 287 NLVQLLGVLILHQ-GLTIVMEHVSKGKGNLVNLFTRGRALVNTAQLOFSLHVAGEYE 344

Db 247 NLVQLLGVLILHQ-GLTIVMEHVSKGKGNLVNLFTRGRALVNTAQLOFSLHVAGEYE 306

QY 345 SKKLVRHDLAARNLILVSSDLVAKVSDGLAKERKGKLDSSRLPVKMTAPEALKHGKPTSK 404

Db 307 GNNFVHROLAARNLILVSNDNAVKVSDGLKTEASSTDTGKLPVKWTAPELREKKFSTK 366

QY 405 SDWWSFGYLWEEFSYRAPSYKMSLKEVEAKVSYRMEPPEGCQGPVHYLMSSWAE 464

Db 367 SDWWSFGYLWEEFSYRAPSYKMSLKEVEAKVSYRMEPPEGCQGPVHYLMSSWAE 426

QY 465 PARRPPFKLAEKL 478

Db 427 AAMRPSFLQLRQEL 440

RESULT 12

Db AAG67444

ID AAG67444 standard; Protein; 450 AA.

XX AC AAG67444;

XX DT 26-NOV-2001 (first entry)

DE Amino acid sequence of a human polypeptide.

XX Human; protein kinase; protein phosphatase; signal transduction; intracellular signalling pathway.

XX KW

XX OS Homo sapiens.

XX PN WO200109345-A1.

XX PD 08-FEB-2001.

XX PF 28-JUL-2000; 2000WO-JP05060.

XX PR 29-JUL-1999; 99JP-0248036.

PR 18-OCT-1999; 99US-0159590.

PR 11-JAN-2000; 2000JP-0118776.

PR 17-FEB-2000; 2000US-0183322.

PR 02-MAY-2000; 2000JP-0183767.

XX PA (HELI-) HELIX RES INST.

XX PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J, Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T, Funahashi S; PI Senoo C, Nezu J;

XX DR WPI; 2001-564736/63.

XX

PT New genes encoding protein kinase and protein phosphatase, useful for identifying modulators which can be used to treat human or animal disorders associated with the expression or function of these enzymes -

XX PS Example 4; Page 249-252; 336pp; Japanese.

XX

CC The specification describes human protein kinase/protein phosphatases. The polypeptides are expected to participate in signal transduction in cells. The kinase phosphatases are connected with intracellular signalling pathways. Antisense oligonucleotides and compounds identified by screening (agonists or antagonists) can be used to

Db 467 FPGDTLVCQFQSKYEHRYKYLENLITDDEEFFENLGLVHAYEADAGLCTQLIKCL 526
Qy 212 RKHGCKTS--AEEELARAGMNLNQHLTGQAQIGGEGFAGVQGYLQGVAVNIKCV 268
Db 527 PKLGKQEFICINSKDFVQDGWVPEABLQRESIGKGEFDYMLGJLIRNEKAVKMLKDEG 586
Qy 269 TAQAFLETAWMKQHENLYVRLGLVIL-HQGLYIYMEHVSKGNLNFTGRGRALVNTA 327
Db 587 AVOKELAESAQMTELEHDDNUFKIGLUVFTSKHLYVTEMSKGSDVYLSRGROHITKK 645
Qy 328 QLOPSLHVABGMEYLESKKLVHDLAAARNTLVSDDLVAKVSDGLAKABRKGDSSRLP 387
Db 647 DQITFAYDTASGMELAKKVVHROJAAVNWLISEDCVAKVSDGSLAKERECYNDVGLP 706
Qy 388 VKWTPEALHGKFWSKDSWSEGYLWEEFSYGRAPYRPMKLVSEAVEKGYMEPE 447
Db 707 IKWIAPEALKNGRFNSKDSWMSGILLWELIYSGRVPYPRILADVVKHVGYKMEAPE 766
Qy 448 GCPGVPHMLSSCWAEPARRPFRKLAEL 478
Db 767 GCPPEIYMMRQWDLNPAKRPTEFABLKVKL 797

Search completed: July 29, 2003, 09:50:57
Job time : 47 secs

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Copyright (c) 1993 - 2003 CompuGen Ltd.	GenCore version 5.1.6		
OM protein - protein search, using sw model			
Run on:	July 29, 2003, 09:47:52 ; Search time 16 Seconds		
Sequence:	(without alignments) 1490.159 Million cell updates/sec		
Title:	US-09-977-261-2		
Perfect score:	2671		
Scoring table:	BLOSUM62		
Gapop 10.0 , Gapext 0.5			
Searched:	127863 seqs, 47026705 residues		
Total number of hits satisfying chosen parameters:	127863		
Minimum DB seq length:	0		
Maximum DB seq length:	200000000		
Post-processing:	Minimum Match 0%		
	Maximum Match 100%		
	Listing first 45 summaries		
Database :	SwissProt_41: *		
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.			
SUMMARIES			
Result No.	Score	Query Match Length DB ID	Description
1	2671	100.0	507 1 MATK_HUMAN
2	2332	87.3	505 1 MATK_MOUSE
3	2221.5	83.2	467 1 MATK_RAT
4	1253.5	46.9	450 1 CSK_CHICK
5	1245.5	46.6	450 1 CSK_HUMAN
6	1242.5	46.5	450 1 CSK_RAT
7	1227.5	46.0	450 1 CSK_MOUSE
8	762.5	28.5	507 1 LCK_CHICK
9	744.5	27.9	508 1 LCK_HUMAN
10	742.5	27.8	508 1 LCK_MOUSE
11	735.5	27.5	526 1 SRC_RSVR
12	734.5	27.5	568 1 SRC_AVISS
13	734	27.5	537 1 SRC_AVIST
14	733	27.4	532 1 SRC_CHICK
15	731.5	27.4	526 1 SRC_AVISI
16	731.5	27.4	587 1 SRC_AVIS2
17	727.5	27.2	523 1 SRC_RSVP
18	727	27.2	535 1 SRC_HUMAN
19	726	27.2	531 1 SRC1_XENLA
20	724.5	27.1	526 1 HCK_HUMAN
21	724.5	27.1	526 1 SRC_RSVHL
22	724	27.1	531 1 SRC2_XENLA
23	724	27.1	1 ABL_DROME
24	723.5	27.1	526 1 SRC_RSVP
25	716.5	26.8	535 1 SRC_RAT
26	716	26.8	501 1 SRK1_SPOLA
27	714	26.7	540 1 SRC_MOUSE
28	713	26.7	506 1 SRK4_SPOLA
29	713	26.7	511 1 LYN_RAT
30	710	26.6	541 1 YES_MOUSE
31	710	26.6	543 1 YES_HUMAN
32	709	26.5	1 FYN_XIPHE
33	707	26.5	1 HCK_MACFA

RESULT 2	
MATK_MOUSE	
ID	STANDARD; . PRT; 505 AA.
NAME	MATK_MOUSE
AC	P41242;
DT	01-FEB-1995 (Rel. 31, Created)
DT	01-FEB-1996 (Rel. 33, Last sequence update)
DT	15-SEP-2003 (Rel. 42, Last annotation update)
DE	Megakaryocyte-associated tyrosine-protein kinase (EC 2.7.1.112)
DE	(Tyrosine-protein kinase CTK) (Protein kinase NTK).
GN	MATK OR CTK OR NTK.
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX	NCBI_TaxID=10090;
RN	[1]
RP	SEQUENCE OF 41-505 FROM N.A.
RC	TISSUE=Brain;
RX	MEDLINE=94195709; PubMed=7511815;
RA	Klagges S., Adam D., Class K., Fargnoli J., Bolen J.B.,
RA	Penhallow R.C.;
RT	CTK: a protein-tyrosine kinase related to csk that defines an enzyme family.;
RL	Proc. Natl. Acad. Sci. U.S.A. 91:2597-2601(1994).
RN	[2]
RP	SEQUENCE FROM N.A.
RC	STRAIN=BALB/C; TISSUE=Thymus;
RX	MEDLINE=94255451; PubMed=8197166;
RA	Chow L.M.L., Jarvis C.D., Hu Q., Nye S.H., Gervais F.G.,
RA	Veillette A., Matis L.A.;
RT	"Ntk: a Csk-related protein-tyrosine kinase expressed in brain and T lymphocytes."
RL	Proc. Natl. Acad. Sci. U.S.A. 91:4975-4979(1994).
RN	[3]
RP	SEQUENCE OF 41-505 FROM N.A.
RC	STRAIN=DDY/STD;
RX	MEDLINE=95206787; PubMed=7898936;
RA	Kaneo Y., Nonoguchi K., Fukuyama H., Takano S., Higashitsuji H.,
RA	Nishiyama H., Takenawa J., Nakayama H., Fujita J.;
RT	"presence of alternative 5', untranslated sequences and identification of cells expressing ctk transcripts in the brain and testis.";
RL	Oncoogene 10:945-952(1995).
CC	-!- FUNCTION: COULD PLAY A SIGNIFICANT ROLE IN THE SIGNAL TRANSDUCTION OF HEMATOPOIETIC CELLS. MAY REGULATE TYROSINE KINASE ACTIVITY OF SRC-FAMILY MEMBERS IN BRAIN BY SPECIFICALLY PHOSPHORYLATING THEIR C-TERMINAL REGULATORY TYROSINE RESIDUE WHICH ACTS AS A NEGATIVE REGULATORY SITE. IT MAY PLAY AN INHIBITORY ROLE IN THE CONTROL OF T-CELL PROLIFERATION.
CC	-!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC	-!- SUBCELLULAR LOCATION: Cytoplasmic (probable).
CC	-!- ALTERNATIVE PRODUCTS:
CC	Event=Alternative splicing; Named isoforms=2;
CC	Name=1; IsoId=P41242-1; Sequence=Displayed;
CC	Name=2; IsoId=P41242-2; Sequence=VSP..004966;
CC	Note=Minor isoform.
CC	-!- TISSUE SPECIFICITY: MOST ABUNDANT IN BRAIN, AND TO A LESSER EXTENT IN THE SPLEEN, THE THYMUS AND THE LIVER. ALSO FOUND IN THE T-CELL LINEAGE.
CC	-!- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. CSK SUBFAMILY.
CC	-!- SIMILARITY: Contains 1 SH2 domain.
CC	-!- SIMILARITY: Contains 1 SH3 domain.
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DR	EMBL; D45243; BAA03199.1; .
DR	EMBL; L27738; AAB5667.1; .
DR	PIR; I48925; I48925.
DR	PIR; 159296; 159296.
DR	HSSP; P11362; IFGK.
DR	MGD; MGI; 94259; Matk.
DR	InterPro; IPR00718; Prot_kinase.
DR	InterPro; IPR00980; SH2.
DR	InterPro; IPR01452; SH3.
DR	InterPro; IPR01245; Tyr_pk kinase.
DR	Pfam; PF00069; pkinase_1.
DR	Pfam; PF00017; SH2_1.
DR	Pfam; PF00018; SH3_1.
DR	PRINTS; PR00401; SH2DOMAIN.
DR	PRINTS; PR00109; TYRKINASE.
DR	PRODOM; P000001; Prot_kinase_1.
DR	PRODOM; P000093; SH2_1.
DR	SMART; SH0025; SH2_1.
DR	SMART; SH00326; SH2_1.
DR	SMART; SH00219; TYRK_1.
DR	PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR	PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR	PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR	PROSITE; PS50002; SH3_1.
DR	KW transferase; Tyrosine-protein kinase; ATP-binding; SH2 domain; KW SH3 domain; Phosphorylation; Alternative splicing.
FT	DOMAIN 61 108 SH3.
FT	DOMAIN 120 209 SH2.
FT	DOMAIN 233 481 PROTEIN KINASE.
FT	NP-BIND 239 247 ATP (BY SIMILARITY).
FT	BINDING 260 260 ATP (BY SIMILARITY).
FT	ACT_SITE 350 350 BY SIMILARITY.
FT	VARSPLIC 43 43 T -> TO (in isoform 2).
FT	CONFLICT 105 106 /FT1->VSP..004966.
SQ	SEQUENCE 505 AA; 56056 MW; HG -> QR IN REF. 2).
Query Match 87.3% Score 2332; DB 1; Length 505; Best Local Similarity 87.2%; Prcd. No. 5.1e-154; Matches 442; Conservative 26; Mismatches 37; Indels 2; Gaps 2; Query 1 MAGROSSLVSHRAFHGCDSAEELPLRVSPRLRWAHPPVPSARMPTRWAPGQICITKENT 60 1 MARRSSRVSNALAFEGWES RDLPRVSPRLFGAWHPAPAAKRNTP RWAPGQICMCKENS 58 Db 61 RPKPGELAFRKGDWVITLACENKSWYRKHTSGEGLAGALREREALADPKLSM 120 59 RPKPGELAFRKGDWVITLACEDKSYRAKHGSQEGGLAAALRHEAGALSTDPKLSM 118 Db 121 PWFHGKISGQBAVQQLQPPEDGLFLYRESARHPGDYVLCISFRGDVHYRVLHDCHLT 180 Db 119 PWFHGKISGQEAQDQQLQPPEDGLFLYRESARHPGDYVLCISFRGDVHYRVLHDCHLT 178 Db 181 DAEAVFCNLMDMVEHYSKDKGAICTKLVRRKKGTSABEELARGWLNQLHQHITGAQ 240 179 DAEAVFCNLMDMVEHYTKDKGAICTKLVRRKKGTSABEELARGWLNQLHQHITGAQ 238 Qy 241 IGEGERGAVIIGEYEGOKVAKWKNIKDVTAGAFLDFTAVMKMHOHENLVRILGIVLHGL 300 239 IGEGERGAVIIGEYEGOKVAKWKNIKDVTAGAFLDFTAVMKMHOHENLVRILGIVLHGL 298 Qy 301 YIVMHEVSKGNLNLVRLTRGFLVTAQQLQFLSLAVAEGMEYLESKVLVHDLARNILV 360 Db 299 YIVMHEVSKGNLNLVRLTRGFLVTAQQLQFLSLAVAEGMEYLESKVLVHDLARNILV 358 Qy 361 SEDLVAKVSDFLGAKAERKGIDSSRLPVKWAPEALKHGFETSKSDVWSFCVLLRMFVSY 420	

RESULT 3

ID	MARK_RAT	STANDARD	PRT;	467 AA.
AC	P41243;			
DT	01-FEB-1995 (Rel. 31, created)			
DT	01-FEB-1995 (Rel. 31, last sequence update)			
DT	28-FEB-2003 (Rel. 41, last annotation update)			
DE	Megakaryocyte-associated tyrosine-protein kinase (EC 2.7.1.112). (Tyrosine-protein kinase CTK) (protein kinase BATK).			
GN	MARK OR CTK OR BATK.			
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OX			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAINS-SPRAGUE-DAWLEY; TISSUE=Hippocampus;			
RX	MEDLINE=95106341; PubMed=7807586;			
RA	Karas I.W., Moran P., Gripp J., Armanini M., Phillips H.S., Goddard A.,			
RA	*Identification and characterization of Batk, a predominantly brain-specific non-receptor protein tyrosine kinase related to Csk.*;			
RL	J. Neurosci. Res. 38:707-715(1994).			
CC	-!- FUNCTION: Could play a significant role in the signal transduction of hematopoietic cells. May regulate tyrosine kinase activity of SRC family members in brain.			
CC	-!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein			
CC	-!- SUBCELLULAR LOCATION: Cyttoplasmic (Probable).			
CC	-!- TISSUE SPECIFICITY: Enriched in lymphoid tissues.			
CC	-!- SIMILARITY: Belongs to the Tyr family of protein kinases. Csk			
CC	-!- SIMILARITY: Subfamily.			
CC	-!- SIMILARITY: Contains 1 SH2 domain.			
CC	-!- SIMILARITY: Contains 1 SH3 domain.			
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CC	[1]			
EMBL; L34542; AA064524.1; -.				
PRTR; 156579; 156579.				
HSSP; P11362; IFGK.				
InterPro; IPR000719; Prot_kinase.				
InterPro; IPR000980; SH2.				
InterPro; IPR01452; SH3.				
InterPro; IPR001245; Tyr_pk kinase.				
InterPro; IPR000569; kinase; 1.				
Pfam; PF00017; SH2; 1.				
Pfam; PF00018; SH3; 1.				
PRINTS; PR00401; SH2DOMAIN.				
PRINTS; PR00109; TYRKINASE.				
ProDom; PD000001; Prot_kinase; 1.				
ProDom; PD000093; SH2; 1.				
SMART; SM00252; SH2; 1.				
SMART; SM00266; SH3; 1.				
SMART; SM00219; TYRK; 1.				
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.				

RESULT 4

ID	CSK_CHICK	STANDARD	PRT;	450 AA.
AC	P412439;			
DT	01-FEB-1995 (Rel. 31, Created)			
DT	01-FEB-1995 (Rel. 31, last sequence update)			
DT	28-FEB-2003 (Rel. 41, last annotation update)			
DE	Tyrosine-protein kinase CSK (EC 2.7.1.112) (C-SRC kinase).			
GN	CSK.			
OS	Gallus gallus (Chicken).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.			
OC	NCBI_TaxID=9031;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	SEQUENCE-Brain;			
RX	MEDLINE=92196083; PubMed=1372437;			
RA	Sabe H., Knudsen B., Okada M., Nada S., Nakagawa H., Hanafusa H.;			
RT	*Molecular cloning and expression of chicken C-terminal Src kinase;			
RT	lack of stable association with c-Src protein*;			
PROC.	Natl. Acad. Sci. U.S.A. 89:2190-2194(1992).			

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CC

DR DR EMBL: X74765; CAB58362.1; --.
 DR DR EMBL: X60114; CAA42713.1; --.
 DR DR EMBL: X59932; CRR42556.1; --.
 DR DR PIR; JH0559; JH0559.
 DR DR PDB; 1CSK; 31-IUL-94.
 DR DR PDB; 1BYG; 14-OCT-99.
 DR DR Generic; HGNC: 2444; CSR.
 DR DR MIM; 124095; --.
 DR GO; GO:0008022; F:protein C-terminus binding activity; TAS.
 DR GO; GO:0004713; F:protein tyrosine kinase activity; TAS.
 DR GO; GO:000074; P:regulation of cell cycle; TAS.
 DR DR InterPro; IPR000719; Prot-Kinase.
 DR DR InterPro; IPR000980; SH2.
 DR DR InterPro; IPR001452; SH3.
 DR DR InterPro; IPR001245; Tyr_Pkinase.
 DR DR Pfam; PF00069; pkinese; 1.
 DR DR Pfam; PF00017; SH2; 1.
 DR DR Pfam; PF00018; SH3; 1.
 DR DR SMART; SMART; SH2D1A.
 DR DR PRINTS; PRO0109; TYRKINASE.
 DR DR PRODom; PRO0001; PROT_Kinase; 1.
 DR DR PRODom; PRO0003; SH2; 1.
 DR DR PRODom; PRO0006; SH3; 1.
 DR DR SMART; SM00326; SH2; 1.
 DR DR SMART; SM00326; SH3; 1.
 DR DR PROSTE; PS000107; PROTEIN_KINASE_ATP; 1.
 DR DR PROSTE; PS000109; PROTEIN_KINASE_TTR; 1.
 DR DR PROSTE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR DR PROSTE; PS50001; SH2; 1.
 DR DR PROSTE; PS50002; SH3; 1.
 KW TRANSFERASE; Tyrosine-Protein kinase; ATP-binding; SH2 domain;
 FT DOMAIN; SH3 domain; Phosphorylation; 3D-structure.
 FT DOMAIN; 9 70 SH3.
 FT DOMAIN; 82 171 SH2.
 FT DOMAIN; 195 449 PROTEIN_KINASE.
 FT NP_BIND 201 209 ATP (BY SIMILARITY).
 FT BINDING 222 222 ATP (BY SIMILARITY).
 FT ACT_SITE 314 314 BY SIMILARITY.
 FT MOD_RES 416 416 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 FT STRAND 12 16 STRAND
 FT STRAND 20 20 STRAND
 FT TURN 25 26 TURN
 FT STRAND 27 27 STRAND
 FT STRAND 30 30 STRAND
 FT TURN 32 33 TURN
 FT STRAND 35 41 STRAND
 FT TURN 45 46 TURN
 FT STRAND 47 51 STRAND
 FT TURN 53 54 TURN
 FT STRAND 57 61 STRAND
 FT TURN 62 63 TURN
 FT STRAND 65 66 STRAND
 SEQUENCE 450 AA; 50704 MW; 431023A8BC54E00C CRC64;

	Query	Match	Score	Length
Qy	47 WAPGTGTCITKCEHTRPKGELAFRKDVYTLIEACNKS ^W RYVKHTSGOBGLAAGALR	106		
Db	8 WPSGTECIAKYNFHGIAEQDLPCKGDLTVAVTKDPNWYKAKNV-GREGIIPANYQ	66		
Matches	235;	Conservative	81;	Mismatches 115; Indels 3; Gaps 2;
Best Local Similarity	54.1%	Score	1245.5;	Length 450;
Length	54.1%	Score	5.9e-79;	Length 450;
No. of Mismatches	115;	Length	5.9e-79;	Length 450;

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RESULT 7

CSK_MOUSE	STANDARD;	PRT;	450 AA.
ID CSK_MOUSE			
AC P41241; Q03143;			
DT 01-FEB-1995 (Rel. 31, Last sequence update)			
DT 15-SEP-2003 (Rel. 42, Last annotation update)			
DE Tyrosine-protein kinase CSK (EC 2.7.1.112) (C-SRC kinase) (Protein-tyrosine kinase MPK-2).			
DE CSK,			
OS Mus musculus (Mouse).			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OC NCBI_TaxID=10090;			
OX [1]			
RN SEQUENCE FROM N.A.			
RC TISSUE=Brain;			
RX MEDLINE=94195739; PubMed=7511815;			
RA Klages S., Adam D., Class K., Farnoli J., Bolen J. B.,			
RA Penhallow R.C.;			
RT "Ctk: a protein-tyrosine kinase related to Csk that defines an enzyme family.", Wilkinson D.G., Charnay P.,			
RT Proc. Natl. Acad. Sci. U.S.A. 91:2597-2601(1994).			
RN [2]			
RP SEQUENCE OF 316-367 FROM N.A.			
RX STRAIN=C57BL/6; TISSUE=Embryonic brain;			
RX MEDLINE=93096434; PubMed=1281307;			
RA Giliardi-Hebenstreit P., Nieto M.A., Frain M., Mattei M.-G.,			
RA Chrestier A., Wilkinson D.G., Charnay P.;			
RT RT expressed in the developing mouse hindbrain.";			
RL Oncogene 7:2499-2506(1992).			
CC -1- FUNCTION: SPECIFICALLY PHOSPHORYLATES A TYROSINE ON THE SRC			
CC -1- KINASE. THIS TYROSINE ACTS AS A NEGATIVE REGULATORY SITE.			
CC -1- CAN ALSO ACT ON THE LYN AND FYN KINASES.			
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein			
CC -1- tyrosine phosphate.			
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Probable).			
CC -1- TISSUE SPECIFICITY: UBIQUITOUS, BUT MOST ABUNDANT IN THYMUS AND			
CC -1- SPLEEN, AS WELL AS IN NEONATAL BRAIN.			
CC -1- SIMILARITY: BELONGS TO THE TIR FAMILY OF PROTEIN KINASES. CSK			
CC -1- SUBFAMILY.			
CC -1- SIMILARITY: Contains 1 SH3 domain.			
CC -1- SIMILARITY: Contains 1 SH3 domain.			
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CC EMBL; 005247; AAA18766; 1; -.			
DR DR			
DR DR			
DR PIR; I4929, I4892.			
DR PDB; 1JEG; 31-OCT-01.			
DR MGI; 80337; Csk.			
DR Inter-Pro; IPR00719; Prot_kinase.			
DR Inter-Pro; IPR00980; SH2.			
DR Inter-Pro; IPR01452; SH3.			
DR Inter-Pro; IPR001245; Tyr_Pkinase.			
DR Pfam; PF00669; Pkinase; 1.			
DR Pfam; PF00017; SH2; 1.			
DR Prints; PR00401; SH2domain.			
DR Prints; PR00109; TYRKINASE.			
DR Prodrom; PD000001; Prot_kinase; 1.			
DR Prodrom; PD00093; SH2; 1.			
DR Prodrom; PD00066; SH2; 1.			
DR SMART; SM00252; SH2; 1.			
DR SMART; SM00316; SH3; 1.			

CC EMBL; X58631; CAA41484; 1; -.

CC PIR; S15094; S15094.

CC PDB; 1K9A; 01-MAY-02.

CC Inter-Pro; IPR00719; Prot_kinase.

CC Inter-Pro; IPR00980; SH2.

CC Inter-Pro; IPR001452; SH3.

CC Inter-Pro; IPR001245; Tyr_Pkinase.

CC Pfam; PF00069; Pkinase; 1.

CC Pfam; PF00017; SH2; 1.

CC Pfam; PF00018; SH3; 1.

CC Prints; PR00401; SH2domain.

CC Prints; PR00109; TYRKINASE.

CC Prodrom; PD000001; Prot_kinase; 1.

CC Prodrom; PD00093; SH2; 1.

CC Prodrom; PD00066; SH2; 1.

CC SMART; SM00252; SH2; 1.

CC SMART; SM00316; SH3; 1.

CC	modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
DR	EMBL: X03533; CAA27234_1; -; DR
DR	EMBL: M12056; AAB59674_1; -; DR
DR	EMBL: X03533; CAA27235_1; ALT-SEQ; DR
DR	EMBL: CAA27236_1; ALT-SEQ; DR
DR	EMBL: M21511; AAA39422_1; ALT-SEQ; DR
DR	EMBL: M18098; AAA39421_1; -; DR
DR	HSSP: P06239; LCK; DR
DR	MGD: MG1_96756; Lck; DR
DR	InterPro: IPR00719; PROT_kinase; DR
DR	InterPro: IPR00980; SH2; DR
DR	InterPro: IPR01452; SH3; DR
DR	InterPro: IPR01245; TYR_pk kinase; DR
DR	Pfam: PF00069; ptkinase; 1; DR
DR	Pfam: PF00017; SH2; 1; DR
DR	PFAM: PF00018; SH3; 1; DR
DR	PRINTS: PR00401; SH2DOMAIN; DR
DR	PRINTS: PR00452; SH3DOMAIN; DR
DR	PRINTS: PR00109; TYRKINASE; DR
DR	ProDom: PD00001; prot_kinase; 1; DR
DR	ProDom: PD00093; SH2; 1; DR
DR	ProDom: PD00066; SH3; 1; DR
DR	SMART: SM00252; SH2; 1; DR
DR	SMART: SM00326; SH3; 1; DR
DR	SMART: SM00219; TYRK; 1; DR
DR	PROSITE: PS00017; PROTEIN_KINASE_ATP; 1; DR
DR	PROSITE: PS00109; PROTEIN_KINASE_TIR; 1; DR
DR	PROSITE: PS50011; PROTEIN_KINASE_DOM; 1; DR
DR	PROSITE: PS50001; SH2; 1; DR
DR	PROSITE: PS50002; SH3; 1; DR
KW	proto-oncogene tyrosine-protein kinase; Phosphorylation; Transferase; ATP-binding; Myristate; SH2 domain; SH3 domain; Palmitate; Lipoprotein.
INT_MET	0 0 PROBABLE.
LIPID	1 1 MYRISTATE (BY SIMILARITY).
LIPID	2 2 PALMITATE.
FT	4 4 PALMITATE.
FT	120 120 SH3.
FT	126 223 SH2.
FT	244 497 PROTEIN KINASE.
NP	258 258 ATP (BY SIMILARITY).
BINDING	272 272 ATP (BY SIMILARITY).
FT	363 363 BY SIMILARITY.
ACT_SITE	393 393 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
MOD_RES	504 504 PHOSPHORYLATION (NEGATIVE REGULATION) (BY SIMILARITY).
FT	268 268 K>N: REDUCED ACTIVITY.
FT	269 269 V>L: REDUCED ACTIVITY.
FT	270 270 A>S: REDUCED ACTIVITY.
FT	271 271 V>A: REDUCED ACTIVITY.
FT	272 272 K>R: LOSS OF ACTIVITY.
FT	273 273 S>N: REDUCED ACTIVITY.
MUTAGEN	274 274 L>M: REDUCED ACTIVITY.
FT	275 275 K>V: REDUCED ACTIVITY.
MUTAGEN	504 504 Y>F: CAUSES THYMIC TUMORS.
FT	282 283 CONFLICT (IN REF. 2).
SQ	508 AA: 57821 MW; E935562498CAF6578 CRC64; SEQUENCE
Query Match	27.9%; Score 744.5; DB 1; Length 508;
Best Local Similarity	38.1%; Pred. No. 3e-44;
Matches	163; Conservative 84; Mismatches 156; Indels 25; gaps 9;
OY	65 GELAFERKGDVVTEILECENKSQWYRHHNTSGQEGLLAAGALREREALSADPKLSTMWFWH 124
DR	77 GDLGFFERGEQLRILE-QSGEWKAGSLTGQEGFPFNFVAKANSILEP-----PWF 128
DR	125 GKIISGEAVQQLQPPD-GFLVRLRSARHGDYIVLCV----SFRDVIHYRLD-G 176
DR	129 KNLSRKDAEROLARGNTHSFLIRESESTAGSFSLSVRDFDONDQCEVKHYKIRNLNG 188
QY	177 HLTIDEAVFCNLMDMVEIYKORGAICTKLVPRKRKGTKSAEELRAGWMILNQHIT 3365
DR	189 GFTYSPRITFPGVPLGLDVLVRYTNAASDGLCKLHDLSVRYTQ---TOKPQPKWNEDEWEVPLK 245
DR	237 LGAQIGEGERGAVLQGEVIGQ-KVAVKNIK-CDVTAQAFLEDETAWTKMHQENHLYRLGV 23-47
DR	246 LVERLQAGQFGEWVGMGYVNGHTKVAVKSLQKGNSNPVPLAEANLMKQDQHPRVLYAV 305
DR	295 ILLHOGLYTVMEHVSKGNLNVFLRTRGRALVNTQOLLOFLSLHVAEGMEYLESSKKLVHDLA 33-46
DR	366 ANAVILVSPDLCKLAKDGLFLARLIEDNETTARREGAKFPKTPWTAPEAINVGTFTIKSDVMSF 425
DR	306 VTOPIPIVITYEMENGLVDFELKTPSGIKLNUVKKLDMQAQIAEGMAFEEQVYIHDRR 365
DR	355 ARNLIVSDELVAKVSYDSGIA---ERGKLDSSRLPVKWTAPALKIGKFTSKSDVWS 410
DR	366 ANAVILVSPDLCKLAKDGLFLARLIEDNETTARREGAKFPKTPWTAPEAINVGTFTIKSDVMSF 425
DR	411 GVLWEVFSYGRAPYPKMSLKEYSEAVEKGYRMPEPPECPGVPVHLMSCWEARPARRPP 470
DR	426 GLILTEIVTHGRIPYPMGNTPEVIONLERGYRMVRPDNCPEELYHLMMLCWKERPEDRPT 485
DR	471 PRKLAEL 478
DR	486 FDYLRSVL 493
DR	RESULT 10
DR	LCK_HUMAN ID LCK_HUMAN STANDARD; PRT; 508 AA.
DR	AC P06239; P07100; 012850; Q96DM4; Q9WY78;
DR	DT 01-JAN-1988 (Rel. 06; Created)
DR	DT 01-FEB-1994 (Rel. 28; Last sequence update)
DR	DT 15-SEP-2003 (Rel. 42; Last annotation update)
DE	DE Proto-oncogene tyrosine protein kinase LCK (EC 2.7.1.112) (P56-LCK)
DE	DE (LCK) (T cell-specific protein-tyrosine kinase).
OS	OS Homo sapiens (Human)
OC	OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC	OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX	OX NCBI_TaxID:9606;
RN	RN [1]
RP	SEQUENCE FROM N.A.
RX	RX MEDLINE=89123626; PubMed=3265417;
RA	RA Perlmutter R.M., Martin J.D., Lewis D.B., Peet R., Ziegler S.F., Wilson C.B.;
RT	RT "Structure and expression of lck transcripts in human lymphoid cells";
RT	RT J. Cell. Biochem. 38:117-126(1988).
RN	RN [2]
RP	SEQUENCE FROM N.A.
RX	RX MEDLINE=87113831; PubMed=3493153;
RA	RA Koga Y., Caccia N., Toyonaga B., Spolski R., Yanagi Y., Yoshihikai Y., Mak T.W.;
RA	RA "A human T cell-specific cDNA clone (YT16) encodes a protein with extensive homology to a family of protein-tyrosine kinases.";
RT	RT Eur. J. Immunol. 16:1643-1646(1986).
RL	RL Eur. J. Immunol. 16:1643-1646(1986).
RN	RN [3]
RP	RP SEQUENCE FROM N.A.
RP	RP MEDLINE=90108697; PubMed=2558056;
RA	RA Rouser E., van Huyn T., de Souza S.L., Lang M.C., Fischer S., Benarous R.;
RT	RT "Structure of the human lck gene: differences in genomic organisation within src-related genes affect only N-terminal exons.";
RL	RL Gene 84:105-113(1989).
DR	DR [4]
RP	RP SEQUENCE FROM N.A., VARIANTS LEU-27; PRO-GLN-LYS-PRO-231 INS; VAL-352 AND LEU-446, AND PHOSPHORYLATION OF TYR-393 AND TYR-504.
RP	RP AND LEU-446, AND PHOSPHORYLATION OF TYR-393 AND TYR-504.
DR	DR TISSUE-Leukemia; MEDLINE=94187714; PubMed=8139546;
DR	DR Wright D.B., Sefton B.M., Kamps M.P.;
DR	DR "Oncogenic activation of the lck protein accompanies translocation of the lck gene in the human HS2 T-cell leukemia.";
RL	RL Mol. Cell. Biol. 14:2429-2437(1994).

RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
 RC TISSUE="leukemic T-cell";
 RX MEDLINE=9608519; PubMed=7495859;
 RA Vogel L.B., Arthur R., Fujita D.J.,
 RT "An aberrant lck mRNA in two human T-cell lines.";
 RL Blochim. Biophys. Acta 1264:168-172(1995).
 RN [6]

RP SEQUENCE FROM N.A.
 RC TISSUE="Lymph."
 RX MEDLINE=22368257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Grouse L.H., Shemesh C.M., Schuler G.D., Klausner R.D., Collins F.S., Wagner L., Schaefer C.P., Bhat N.K., Aitschui S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Blatckeno L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Donaldson M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Reha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mulilahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Munoz D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Boulard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Kryzwicki M.I., Skalska U., Smialius D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences"; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [7]

RP SEQUENCE OF 13-508 FROM N.A.
 RC TISSUE="Peripheral blood lymphocytes";
 RX MEDLINE=20462621; PubMed=11090907;
 RA Boncristiano M., Majolani M.B., D'Elia M.M., Pacini S., Valensin S., Baldari C.T.; "Defective recruitment and activation of ZAP-70 in common variable immunodeficiency Patients with T cell defects"; Eur. J. Immunol. 30:2632-2638(2000).
 RN [8]

RP SEQUENCE OF 367-508 FROM N.A.
 RX MEDLINE=88217332; PubMed=2835736;
 RA Vilella A., Foss F.M., Sausville E.A., Bolen J.B., Rosen N.; RT "Expression of the lck tyrosine kinase gene in human colon carcinoma and other non-lymphoid human tumor cell lines"; Oncoogene Res. 1:357-374(1987).
 RN [9]

RP SEQUENCE OF 374-508 FROM N.A.
 RX MEDLINE=87000726; PubMed=3489486;
 RA Trevillyan J.M., Lin Y., Chen S.J., Phillips C.A., Canna C., Liina T.J.; RT "Human T-lymphocytes express a protein-tyrosine kinase homologous to p56LSTR"; Blochim. Biophys. Acta 888:286-295(1986).
 RN [10]

RP SEQUENCE OF 1-34 FROM N.A.
 RX MEDLINE=89096891; PubMed=8505079;
 RA Garvin A.M., Pawar S., March J.D., Perlmutter R.M.; RT "Structure of the murine lck gene and its rearrangement in a murine lymphoma cell line"; Mol. Cell. Biol. 8:3058-3064(1988).
 RA "Structure of the two promoters of the human lck gene: differential accumulation of two classes of lck transcripts in T cells"; Mol. Cell. Biol. 9:2173-2180(1989).
 RN [11]

RP SEQUENCE OF 1-34 FROM N.A.
 RX MEDLINE=8913764; PubMed=2787474;
 RA Takadera T., Leung S., Germino A., Koga Y., Takihara Y., Miyamoto N.G., Mak T.W.; RT "Structure of the two promoters of the human lck gene: differential accumulation of two classes of lck transcripts in T cells"; Mol. Cell. Biol. 9:2173-2180(1989).
 RN [12]

RP MASS SPECTROMETRY.
 RC TISSUE="breast cancer";

RX MEDLINE=21829512; PubMed=11840567;
 RA Harris R.A., Yang A., Stein R.C., Lucy K., Brusten L., Herath A., Parekh R., Waterfield M.D., O'Hare M.J., Neville M.A., Page M.J., Zveibil M.J.; RT "Cluster analysis of an extensive human breast cancer cell line protein expression map database"; RL Proteomics 2:212-223(2002).
 RN [13]

RP INTERACTION WITH PI3K.
 RX MEDLINE=94067101; PubMed=7504174;
 RA Vogel L.B., Fujita D.J.; RT "The SH3 domain of p56lck is involved in binding to phosphatidylinositol 3'-kinase from T lymphocytes"; Mol. Cell. Biol. 13:7408-7417(1993).
 RN [14]

RP INTERACTION WITH KHDRBS1.
 RX MEDLINE=95155308; PubMed=7852312;
 RA Vogel L.B., Fujita D.J.; RT "p10 phosphorylation and binding to p56lck is an early event in interleukin-2-induced onset of cell cycle progression in T-lymphocytes"; J. Biol. Chem. 270:2506-2511(1995).
 RN [15]

RP PHOSPHORYLATION OF TYR-504.
 RX MEDLINE=9237326; PubMed=1639064;
 RA Bergman M., Mustelin T., Oetken C., Partanen J., Flint N.A., Areuin K.E., Autero M., Burn P., Alitalo K.; RT "The human p50csk tyrosine kinase phosphorylates p56lck at Tyr-505 and down regulates its catalytic activity"; EMBO J. 11:2919-2924(1992).
 RN [16]

RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 52-225.
 RX MEDLINE=94203291; PubMed=7512222;
 RA Eck M.J., Atweel S.K., Shoelson S.E., Harrison S.C.; RT "Structure of the regulatory domains of the Src-family tyrosine kinase lck"; Nature 368:764-769(1994).
 RN [17]

RP X-RAY CRYSTALLOGRAPHY (2.25 ANGSTROMS) OF 126-220.
 RX MEDLINE=95173978; PubMed=7532720;
 RA Mikol V., Baumann G., Keller T.H., Manning U.M., Zurini M.G.M.; RT "The crystal structures of the SH2 domain of p56lck complexed with two phosphopeptides suggest a gated peptide binding site"; J. Mol. Biol. 246:344-355(1995).
 RN [18]

RP X-RAY CRYSTALLOGRAPHY (1.0 ANGSTROMS) OF 121-225.
 RX MEDLINE=96177765; PubMed=8804142;
 RA Tong L., Warren T.C., King J., Betageri R., Rose J., Jakes S.; RT "Crystal structures of the human p56lck SH2 domain in complex with two short phosphotyrosyl peptides at 1.0-A and 1.8-A resolution"; J. Mol. Biol. 256:601-610(1996).
 RN [19]

RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 118-225.
 RX MEDLINE=9832059; PubMed=9885372;
 RA Tong L., Warren T.C., Lukas S., Schembri-King J., Betageri R., Proudfoot J.R., Jakes S.; RT "Carboxymethyl-phenylalanine as a replacement for phosphotyrosine in SH2 domain binding"; J. Biol. Chem. 273:20238-20242(1998).
 RN [20]

RP X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS) OF 230-500.
 RX MEDLINE=9710052; PubMed=8845479;
 RA Yamaguchi H., Hendrickson W.A.; RT "Structural basis for activation of human lymphocyte kinase Lck upon tyrosine phosphorylation"; Nature 384:484-489(1996).
 RN [21]

RP X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS) OF 230-500.
 RX MEDLINE=9710052; PubMed=8845479;
 RA Yamaguchi H., Hendrickson W.A.; RT "Structural basis for activation of human lymphocyte kinase Lck upon tyrosine phosphorylation"; Nature 384:484-489(1996).
 RN [22]

CC -1 FUNCTION: MAY PARTICIPATE IN ANTIGEN-INDUCED T-CELL ACTIVATION.
 CC -1 CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC -1 tyrosine phosphate.
 CC -1 SUBUNIT: Binds to phosphatidylinositol 3'-kinase (PI3K) from T lymphocytes through its SH3 domain and to the tyrosine phosphorylated form of KHDRBS1/p70 through its SH2 domain.
 CC -1 SUBCELLULAR LOCATION: BOUND TO THE CYTOPLASMIC DOMAIN OF EITHER

DR	InterPro; IPR01452; SH3.	236	TIGAQIGEGERGAVLQGYLG-QKVAVKNIK-CDVTAQAFQALDDETAVMTKMHENLVRLIG
DR	InterPro; IPR01245; Tyr_Pkinase.	268	RLEVKIGQGCYGEWMMGWTWNSGTRVAKTLKGTMSSBAAQFLQVMMKKLRRKLVQY
Pfam	PF00017; SH2; 1.	409	PFAM; PF00017; SH2; 1.
Pfam	PF00018; SH3; 1.	377	PFAM; PF00018; SH3; 1.
PRINTS	PR00452; SH3DOMAIN.	353	PRINTS; PR00452; SH3DOMAIN.
PRINTS	PR0109; TYRKINASE.	387	PRINTS; PR0109; TYRKINASE.
PRODOM	PD000001; Prot_kinase; 1.	354	PRODOM; PD000001; Prot_kinase; 1.
PRODOM	PD000093; SH2; 1.	409	PRODOM; PD000093; SH2; 1.
PRODOM	PD000056; SH3; 1.	447	PRODOM; PD000056; SH3; 1.
SMART	SM00252; SH2; 1.	470	SMART; SM00252; SH2; 1.
SMART	SM00326; SH3; 1.	470	SMART; SM00326; SH3; 1.
PROSITE	PS00107; PROTEIN_KINASE_ATP; 1.	470	PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE	PS00109; PROTEIN_KINASE_TYR; 1.	507	PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
PROSITE	PS50011; PROTEIN_KINASE_DOM; 1.	507	PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR	PS50001; SH2; 1.	507	DR; PS50001; SH2; 1.
DR	PS50002; SH3; 1.	507	DR; PS50002; SH3; 1.
KW	Tyrosine-protein kinase; Oncogene; Transferase; Phosphorylation; ATP-binding; Myristate; SH3 domain; SH2 domain; 3D-structure.	508	TFFEYLGQQL 516
FT	LIPID	508	
FT	ATP DOMAIN	81	SH3.
FT	DOMAIN	148	SH2.
FT	DOMAIN	245	PROTEIN KINASE.
FT	NP_BIND	273	ATP (BY SIMILARITY):
FT	BINDING	295	ATP (BY SIMILARITY).
FT	ACT_SITE	386	BY SIMILARITY.
FT	MOD_RES	416	PHOSPHORYLATION (AUTO-).
FT	CONFFLICT	10	G -> D (IN REF. 2 AND 3).
FT	CONFFLICT	63	D -> G (IN REF. 2).
FT	CONFFLICT	96	I -> T (IN REF. 3).
FT	CONFFLICT	124	V -> L (IN REF. 2).
FT	CONFFLICT	301	T -> N (IN REF. 3).
K	-> E (IN REF. 2 AND 3).	410	PGVLLMEVFSVGRAPYPKMSKKEVSEAVKEGYRMRMPCPPECPSLHDMSQWRDPERP
S	-> C (IN REF. 2 AND 3).	448	PGILLTELTTRGKRVPGMNGEVLDRVERGVRMPCPPECPSLHDMSQWRDPERP
RESULT 12	508 TFFEYLGQQL 516	470	PFRKLAELK 478
SRC_AVISS		508	
ID		508	
AC		508	
PI4084;		508	
DT	01-JAN-1990 (Ref. 13. Created)	508	
DT	01-JAN-1990 (Ref. 13. Last sequence update)	508	
DT	28-FEB-2003 (Ref. 41. Last annotation update)	508	
DE	Tyrosine-protein kinase transforming protein SRC (EC 2.7.1.112) (P60- SRC).	508	
DE	V-SRC.	508	
GN		508	
OS	Avian sarcoma virus (strain S1).	508	
OC	Viruses; Retrovirusidae; Avian type C retroviruses.	508	
OX	NCBI_TaxID:11881.	508	
RN	[1]	508	
RP	SEQUENCE FROM N.A.	508	
RX	MEDLINE=87064539; PubMed=3097513;	508	
RA	Ikawa S., Hagiwano-Yamagishi K., Kawai S., Yamamoto T., Toyoshima K.; "Activation of the cellular src gene by transducing retrovirus.";	508	
RT	Cell. Biol. 6:420-428(1986).	508	
RL	Mol. Cell. Biol. 6:420-428(1986).	508	
CC	-I FUNCTION: THIS PROSHPROTEIN, REQUIRED FOR BOTH THE INITIATION AND THE MAINTENANCE OF NEOPLASTIC TRANSFORMATION, IS A PROTEIN KINASE THAT CATALYZES THE PHOSPHORYLATION OF TYROSINE RESIDUES IN VITRO.	508	
CC	-I CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein tyrosine phosphate.	508	
CC	-I SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. SRC SUBFAMILY.	508	
CC	-I SIMILARITY: Contains 1 SH2 domain.	508	
CC	-I SIMILARITY: Contains 1 SH3 domain.	508	
DR	HSSP; P00523; 2PTK.	508	
DR	InterPro; IPR000719; Prot_kinase.	508	
DR	InterPro; IPR000980; SH2.	508	
DR	InterPro; IPR01452; SH3.	508	
DR	InterPro; IPR01245; Tyr_Pkinase.	508	
DR	Pfam; PF00069; kinase; 1.	508	
DR	Pfam; PF00017; SH2; 1.	508	
DR	Pfam; PF00018; SH3; 1.	508	
DR	PRINTS; PR00401; SH3DOMAIN.	508	
DR	PRINTS; PR00452; SH3DOMAIN.	508	
DR	PRINTS; PR00109; TYRKINASE.	508	
DR	PRODOM; PD000001; Prot_kinase; 1.	508	
DR	PRODOM; PD000093; SH2; 1.	508	
DR	PRODOM; PD000066; SH3; 1.	508	
DR	SMART; SM00252; SH2; 1.	508	
DR	SMART; SM00326; SH3; 1.	508	
DR	SMART; SM00219; TYRK; 1.	508	
PROSITE	PS00107; PROTEIN_KINASE_ATP; 1.	508	
PROSITE	PS00109; PROTEIN_KINASE_TYR; 1.	508	
PROSITE	PS50011; PROTEIN_KINASE_DOM; 1.	508	
PROSITE	PS50001; SH2; 1.	508	
DB	PS50002; SH3; 1.	508	
DB	PS50003; SH2; 1.	508	
DB	PS50004; SH3; 1.	508	
DB	PS50005; SH2; 1.	508	
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DB	PS50216; SH3; 1.	508	
DB	PS50217; SH2; 1.	508	
DB	PS50218; SH3; 1.	508	

KW	Tyrosine-protein kinase; Oncogene; transferase; Phosphorylation;	CC	tyrosine phosphate.
ATP-binding; Myristate; SH3 domain; SH2 domain.	CC	- I - SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. SRC	
LIPID	CC	SUBFAMILY.	
DOMAIN	CC	- I - SIMILARITY: Contains 1 SH2 domain.	
148	CC	- I - SIMILARITY: Contains 1 SH3 domain.	
245	CC	- I - SIMILARITY: Contains 1 SH3 domain.	
267	CC	- I - SIMILARITY: Contains 1 SH3 domain.	
NP-BIND	DR	DR	
273	DR	HSSP; P00533; 2P9K.	
BINDING	DR	InterPro; IPR00719; prot_kinase.	
295	DR	InterPro; IPR00980; SH2.	
ACT-SITE	DR	InterPro; IPR01452; SH3.	
386	DR	InterPro; IPR01245; Tyr_Pkinase.	
MOD-RES	DR	InterPro; IPR0069; Pkinase; 1.	
416	DR	Pfam; PF00017; SH2; 1.	
SEQUENCE	DR	Pfam; PF00018; SH3; 1.	
63632 MW;	DR	PRINTS; PRO0401; SH2DOMAIN.	
13777DB121F70938 CRC64;	DR	PRINTS; PRO0452; SH3DOMAIN.	
Qy	DR	PRINTS; PRO0119; TRKINASE.	
66	DR	PRODOM; PD000093; SH2; 1.	
ELAFRKGVVTLACENKSMWYRKHITSQGQGLAAGALRREALSADPKLISLMPWFHG	DR	PRODOM; PD000066; SH3; 1.	
99	DR	SMART; SM00326; SH2; 1.	
DLSFKKGGERLQTYNNTBG-DWMLAHSLTGONGYIPSNYVAPSDSTOAE-----ENYFG	DR	SMART; SM003219; TYK2; 1.	
125	DR	PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.	
178	DR	PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.	
LTIDEEAVFCNLMDVMEYISKORGATCKL-VRPKRKHGTSAEELRAGWLNLIQHL	DR	PROSITE; PS50001; PROTEIN_KINASE_DOM; 1.	
212	DR	PROSITE; PS50001; SH2; 1.	
FITSRQFSSQQLQVAVYTSKHDGLCHRLTNVCPISKPKQIG---LAKDWEIPRESL	DR	PROSITE; PS50001; SH3; 1.	
236	DR	PROSITE; PS50002; SH3; 1.	
TLGAQIGERGEGFQAVLQSYLQ-OKVAVKNK-CDVTAQAFELDETAVMTKMOHENLYLIG	DR	PROSITE; PS50002; SH3; 1.	
268	DR	PROSITE; PS50002; SH3; 1.	
RLEVKGCGFCGEWMMGTTWNGTTRVAIKTLPGTMSPAFQALQBAQMKLKRHEKLYLA	DR	PROSITE; PS50002; SH3; 1.	
294	DR	PROSITE; PS50002; SH3; 1.	
VLRQGLYIVMEHVSKGKLNVLNTRGRALVTAQQLQFSLHVAEGMEYLESKKVHLRDL	DR	PROSITE; PS50002; SH3; 1.	
353	DR	PROSITE; PS50002; SH3; 1.	
328	DR	PROSITE; PS50002; SH3; 1.	
VVSEEPITVTEYMSKSLDPLKGEMGKYLRLPQDMAQIASGHWAYVERMVYVHDL	DR	PROSITE; PS50002; SH3; 1.	
387	DR	PROSITE; PS50002; SH3; 1.	
354	DR	PROSITE; PS50002; SH3; 1.	
AARNILYSEDLYAVSKDGLAKA---ERKGIDSSRPLPKWTAPEALKHGKFTSKDWS	DR	PROSITE; PS50002; SH3; 1.	
409	DR	PROSITE; PS50002; SH3; 1.	
388	DR	PROSITE; PS50002; SH3; 1.	
RAANILYGENLIVCKVADPLGLARIEDNEYTAQGAKPKIWKTAPEALKHGKFTSKDWS	DR	PROSITE; PS50002; SH3; 1.	
447	DR	PROSITE; PS50002; SH3; 1.	
Qy	DR	PROSITE; PS50002; SH3; 1.	
410	DR	PROSITE; PS50002; SH3; 1.	
FGVLLWEVFSYGRAPYKMSLKEVEAEGYTRMEPEPGCPGPVHIMSSWEAEARRP	DR	PROSITE; PS50002; SH3; 1.	
469	DR	PROSITE; PS50002; SH3; 1.	
448	DR	PROSITE; PS50002; SH3; 1.	
FGILLTEITTKGRVVPQGMVNREVLDQVERGYRMPCPPECPELSDHLMQCRWDPEERP	DR	PROSITE; PS50002; SH3; 1.	
507	DR	PROSITE; PS50002; SH3; 1.	
Db	DR	PROSITE; PS50002; SH3; 1.	
508	DR	PROSITE; PS50002; SH3; 1.	
RESULT 13	DR	PROSITE; PS50002; SH3; 1.	
SRC_AVIST	DR	PROSITE; PS50002; SH3; 1.	
ID	DR	PROSITE; PS50002; SH3; 1.	
SRC_AVIST	DR	PROSITE; PS50002; SH3; 1.	
STANDARD;	DR	PROSITE; PS50002; SH3; 1.	
PRT;	DR	PROSITE; PS50002; SH3; 1.	
557 AA.	DR	PROSITE; PS50002; SH3; 1.	
Qy	DR	PROSITE; PS50002; SH3; 1.	
66	DR	PROSITE; PS50002; SH3; 1.	
ELAFRKGVVTLACENKSMWYRKHITSQGQGLAAGALRREALSADPKLISLMPWFHG	DR	PROSITE; PS50002; SH3; 1.	
99	DR	PROSITE; PS50002; SH3; 1.	
DLSFKKGGERLQTYNNTBG-DWMLAHSLTGONGYIPSNYVAPSDSTOAE-----ENYFG	DR	PROSITE; PS50002; SH3; 1.	
125	DR	PROSITE; PS50002; SH3; 1.	
178	DR	PROSITE; PS50002; SH3; 1.	
LTIDEEAVFCNLMDVMEYISKORGATCKL-VRPKRKHGTSAEELRAGWLNLIQHL	DR	PROSITE; PS50002; SH3; 1.	
235	DR	PROSITE; PS50002; SH3; 1.	
212	DR	PROSITE; PS50002; SH3; 1.	
FITSRQFSSQQLQVAVYTSKHDGLCHRLTNVCPISKPKQIG---LAKDWEIPRESL	DR	PROSITE; PS50002; SH3; 1.	
267	DR	PROSITE; PS50002; SH3; 1.	
354	DR	PROSITE; PS50002; SH3; 1.	
AARNILYSEDLYAVSKDGLAKA---ERKGIDSSRPLPKWTAPEALKHGKFTSKDWS	DR	PROSITE; PS50002; SH3; 1.	
409	DR	PROSITE; PS50002; SH3; 1.	
388	DR	PROSITE; PS50002; SH3; 1.	
RAANILYGENLIVCKVADPLGLARIEDNEYTAQGAKPKIWKTAPEALKHGKFTSKDWS	DR	PROSITE; PS50002; SH3; 1.	
447	DR	PROSITE; PS50002; SH3; 1.	
Qy	DR	PROSITE; PS50002; SH3; 1.	
66	DR	PROSITE; PS50002; SH3; 1.	
ELAFRKGVVTLACENKSMWYRKHITSQGQGLAAGALRREALSADPKLISLMPWFHG	DR	PROSITE; PS50002; SH3; 1.	
99	DR	PROSITE; PS50002; SH3; 1.	
DLSFKKGGERLQTYNNTBG-DWMLAHSLTGONGYIPSNYVAPSDSTOAE-----ENYFG	DR	PROSITE; PS50002; SH3; 1.	
125	DR	PROSITE; PS50002; SH3; 1.	
178	DR	PROSITE; PS50002; SH3; 1.	
LTIDEEAVFCNLMDVMEYISKORGATCKL-VRPKRKHGTSAEELRAGWLNLIQHL	DR	PROSITE; PS50002; SH3; 1.	
235	DR	PROSITE; PS50002; SH3; 1.	
212	DR	PROSITE; PS50002; SH3; 1.	
FITSRQFSSQQLQVAVYTSKHDGLCHRLTNVCPISKPKQIG---LAKDWEIPRESL	DR	PROSITE; PS50002; SH3; 1.	
267	DR	PROSITE; PS50002; SH3; 1.	
354	DR	PROSITE; PS50002; SH3; 1.	
AARNILYSEDLYAVSKDGLAKA---ERKGIDSSRPLPKWTAPEALKHGKFTSKDWS	DR	PROSITE; PS50002; SH3; 1.	
409	DR	PROSITE; PS50002; SH3; 1.	
388	DR	PROSITE; PS50002; SH3; 1.	
RAANILYGENLIVCKVADPLGLARIEDNEYTAQGAKPKIWKTAPEALKHGKFTSKDWS	DR	PROSITE; PS50002; SH3; 1.	
447	DR	PROSITE; PS50002; SH3; 1.	
Qy	DR	PROSITE; PS50002; SH3; 1.	
410	DR	PROSITE; PS50002; SH3; 1.	
FGVLLWEVFSYGRAPYKMSLKEVEAEGYTRMEPEPGCPGPVHIMSSWEAEARRP	DR	PROSITE; PS50002; SH3; 1.	
469	DR	PROSITE; PS50002; SH3; 1.	
448	DR	PROSITE; PS50002; SH3; 1.	
FGILLTEITTKGRVVPQGMVNREVLDQVERGYRMPCPPECPELSDHLMQCRWDPEERP	DR	PROSITE; PS50002; SH3; 1.	
507	DR	PROSITE; PS50002; SH3; 1.	
Db	DR	PROSITE; PS50002; SH3; 1.	
508	DR	PROSITE; PS50002; SH3; 1.	
512	DR	PROSITE; PS50002; SH3; 1.	
Qy	DR	PROSITE; PS50002; SH3; 1.	
66	DR	PROSITE; PS50002; SH3; 1.	
ELAFRKGVVTLACENKSMWYRKHITSQGQGLAAGALRREALSADPKLISLMPWFHG	DR	PROSITE; PS50002; SH3; 1.	
99	DR	PROSITE; PS50002; SH3; 1.	
DLSFKKGGERLQTYNNTBG-DWMLAHSLTGONGYIPSNYVAPSDSTOAE-----ENYFG	DR	PROSITE; PS50002; SH3; 1.	
125	DR	PROSITE; PS50002; SH3; 1.	
178	DR	PROSITE; PS50002; SH3; 1.	
LTIDEEAVFCNLMDVMEYISKORGATCKL-VRPKRKHGTSAEELRAGWLNLIQHL	DR	PROSITE; PS50002; SH3; 1.	
235	DR	PROSITE; PS50002; SH3; 1.	
212	DR	PROSITE; PS50002; SH3; 1.	
FITSRQFSSQQLQVAVYTSKHDGLCHRLTNVCPISKPKQIG---LAKDWEIPRESL	DR	PROSITE; PS50002; SH3; 1.	
267	DR	PROSITE; PS50002; SH3; 1.	
354	DR	PROSITE; PS50002; SH3; 1.	
AARNILYSEDLYAVSKDGLAKA---ERKGIDSSRPLPKWTAPEALKHGKFTSKDWS	DR	PROSITE; PS50002; SH3; 1.	
409	DR	PROSITE; PS50002; SH3; 1.	
388	DR	PROSITE; PS50002; SH3; 1.	
RAANILYGENLIVCKVADPLGLARIEDNEYTAQGAKPKIWKTAPEALKHGKFTSKDWS	DR	PROSITE; PS50002; SH3; 1.	
447	DR	PROSITE; PS50002; SH3; 1.	
Qy	DR	PROSITE; PS50002; SH3; 1.	
410	DR	PROSITE; PS50002; SH3; 1.	
FGVLLWEVFSYGRAPYKMSLKEVEAEGYTRMEPEPGCPGPVHIMSSWEAEARRP	DR	PROSITE; PS50002; SH3; 1.	
469	DR	PROSITE; PS50002; SH3; 1.	
448	DR	PROSITE; PS50002; SH3; 1.	
FGILLTEITTKGRVVPQGMVNREVLDQVERGYRMPCPPECPELSDHLMQCRWDPEERP	DR	PROSITE; PS50002; SH3; 1.	
507	DR	PROSITE; PS50002; SH3; 1.	
Db	DR	PROSITE; PS50002; SH3; 1.	
508	DR	PROSITE; PS50002; SH3; 1.	
512	DR	PROSITE; PS50002; SH3; 1.	
Qy	DR	PROSITE; PS50002; SH3; 1.	
470	DR	PROSITE; PS50002; SH3; 1.	
PERKL	DR	PROSITE; PS50002; SH3; 1.	
474	DR	PROSITE; PS50002; SH3; 1.	
Db	DR	PROSITE; PS50002; SH3; 1.	
508	DR	PROSITE; PS50002; SH3; 1.	
512	DR	PROSITE; PS50002; SH3; 1.	
Qy	DR	PROSITE; PS50002; SH3; 1.	
470	DR	PROSITE; PS50002; SH3; 1.	
PERKL	DR	PROSITE; PS50002; SH3; 1.	
474	DR	PROSITE; PS50002; SH3; 1.	
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508	DR	PROSITE; PS50002; SH3; 1.	
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Qy	DR	PROSITE; PS50002; SH3; 1.	
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PERKL	DR	PROSITE; PS50002; SH3; 1.	
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Qy	DR	PROSITE; PS50002; SH3; 1.	
470	DR	PROSITE; PS50002; SH3; 1.	
PERKL	DR	PROSITE; PS50002; SH3; 1.	
474	DR	PROSITE; PS50002; SH3; 1.	
Db	DR	PROSITE; PS50002; SH3; 1.	
508	DR	PROSITE; PS50002; SH3; 1.	
512	DR	PROSITE; PS50002; SH3; 1.	
Qy	DR	PROSITE; PS50002; SH3; 1.	
470	DR	PROSITE; PS50002; SH3; 1.	
PERKL	DR	PROSITE; PS50002; SH3; 1.	
474	DR	PROSITE; PS50002; SH3; 1.	
Db	DR	PROSITE; PS50002; SH3; 1.	
508	DR	PROSITE; PS50002; SH3; 1.	
512	DR	PROSITE; PS50002; SH3; 1.	
Qy	DR	PROSITE; PS50002; SH3; 1.	
470	DR	PROSITE; PS50002; SH3; 1.	
PERKL	DR	PROSITE; PS50002; SH3; 1.	
474	DR	PROSITE; PS50002; SH3; 1.	
Db	DR	PROSITE; PS50002; SH3; 1.	
508	DR	PROSITE; PS50002; SH3; 1.	
512	DR	PROSITE; PS50002; SH3; 1.	
Qy	DR	PROSITE; PS50002; SH3; 1.	
470	DR	PROSITE; PS50002; SH3; 1.	
PERKL	DR	PROSITE; PS50002; SH3; 1.	
474	DR	PROSITE; PS50002; SH3; 1.	
Db	DR	PROSITE; PS50002; SH3; 1.	
508	DR	PROSITE; PS50002; SH3; 1.	
512	DR	PROSITE; PS50002; SH3; 1.	
Qy	DR	PROSITE; PS50002; SH3; 1.	
470	DR	PROSITE; PS50002; SH3; 1.	
PERKL	DR	PROSITE; PS50002; SH3; 1.	
474	DR	PROSITE; PS50002; SH3; 1.	
Db	DR	PROSITE; PS50002; SH3; 1.	
508	DR	PROSITE; PS50002; SH3; 1.	
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470	DR	PROSITE; PS50002; SH3; 1.	
PERKL	DR	PROSITE; PS50002; SH3; 1.	
474	DR	PROSITE; PS50002; SH3; 1.	
Db	DR	PROSITE; PS50002; SH3; 1.	
508	DR	PROSITE; PS50002; SH3; 1.	
512	DR	PROSITE; PS50002; SH3; 1.	
Qy	DR	PROSITE; PS50002; SH3; 1.	
470	DR	PROSITE; PS50002; SH3; 1.	
PERKL	DR	PROSITE; PS50002; SH3; 1.	
474	DR	PROSITE; PS50002; SH3; 1.	
Db	DR	PROSITE; PS50002; SH3; 1.	
508	DR	PROSITE; PS50002; SH3; 1.	
512	DR	PROSITE; PS50002; SH3; 1.	
Qy	DR	PROSITE; PS50002; SH3; 1.	
470	DR	PROSITE; PS50002; SH3; 1.	
PERKL	DR	PROSITE; PS50002; SH3; 1.	
474	DR	PROSITE; PS50002; SH3; 1.	
Db	DR	PROSITE; PS50002; SH3; 1.	
508	DR	PROSITE; PS50002; SH3; 1.	
512	DR	PROSITE; PS50002; SH3; 1.	
Qy	DR	PROSITE; PS50002; SH3; 1.	
470	DR	PROSITE; PS50002; SH3; 1.	
PERKL	DR	PROSITE; PS50002; SH3; 1.	
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Qy	DR	PROSITE; PS50002; SH3; 1.	
470	DR	PROSITE; PS50002; SH3; 1.	
PERKL	DR	PROSITE; PS50002; SH3; 1.	
474	DR	PROSITE; PS50002; SH3; 1.	
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Qy	DR	PROSITE; PS50002; SH3; 1.	
470	DR	PROSITE; PS50002; SH3; 1.	
PERKL	DR	PROSITE; PS50002; SH3; 1.	
474	DR	PROSITE; PS50002; SH3; 1.	
Db	DR	PROSITE; PS50002; SH3; 1.	
508	DR	PROSITE; PS50002; SH3; 1.	
512	DR	PROSITE; PS50002; SH3; 1.	
Qy	DR	PROSITE; PS50002; SH3; 1.	
470	DR	PROSITE; PS50002; SH3; 1.	
PERKL	DR	PROSITE; PS50002; SH3; 1.	
474	DR	PROSITE; PS50002; SH3; 1.	
Db	DR	PROSITE; PS50002; SH3; 1.	
508	DR	PROSITE; PS50002; SH3; 1.	
512	DR	PROSITE; PS50002; SH3; 1.	
Qy	DR	PROSITE; PS50002; SH3; 1.	
470	DR	PROSITE; PS50002; SH3; 1.	
PERKL	DR	PROSITE; PS50002; SH3; 1.	
474	DR	PROSITE; PS50002; SH3; 1.	
Db	DR	PROSITE; PS50002; SH3; 1.	
508	DR	PROSITE; PS50002; SH3; 1.	
512	DR	PROSITE; PS50002; SH3; 1.	
Qy	DR	PROSITE; PS50002; SH3; 1.	
470	DR	PROSITE; PS50002; SH3; 1.	
PERKL	DR	PROSITE; PS50002; SH3; 1.	
474	DR	PROSITE; PS50002; SH3; 1.	
Db	DR	PROSITE; PS50002; SH3; 1.	
508	DR	PROSITE; PS50002; SH3; 1.	
512	DR	PROSITE; PS50002; SH3; 1.	
Qy	DR	PROSITE; PS50002; SH3; 1.	
470	DR	PROSITE; PS50002; SH3; 1.	
PERKL	DR	PROSITE; PS50002; SH3; 1.	
474	DR	PROSITE; PS50002; SH3; 1.	
Db	DR	PROSITE; PS50002; SH3; 1.	
508	DR	PROSITE; PS50002; SH3; 1.	
512	DR	PROSITE; PS50002; SH3; 1.	
Qy	DR	PROSITE; PS50002; SH3; 1.	
470	DR	PROSITE; PS50002; SH3; 1.	
PERKL	DR	PROSITE; PS50002; SH3; 1.	
474	DR	PROSITE; PS50002; SH3; 1.	
Db	DR	PROSITE; PS50002; SH3; 1.	
508	DR	PROSITE; PS50002; SH3; 1.	

Db 508 TFEYLQAFLEDYLGLAWTPWEDKQEGPRGETASNKQE 545

RA Cooper J.A., Gould K.L., Cartwright C.A., Hunter T.;
RT "Tyr27 is phosphorylated in pp60c-src: implications for regulation.";
RN Science 231:1431-1434(1986).

RESULT 14

SRC_CHICK STANDARD PRT; 532 AA.

ID P0053; Q90992; Q91343; Q91345; Q92013; Q98915;

AC P0053; Q90992; Q91343; Q91345; Q92013; Q98915;

DT 21-JUL-1986 (Rel. 01, Created)

DT 15-JUL-1999 (Rel. 38, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE Proto-oncogene tyrosine-protein kinase SRC (EC 2.7.1.112) (p60-Src)

DE (c-Src).

GN SRC.

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Archosauvia; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

OC Gallus.

OX NCBI_TAXID=9031;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=83155664; PubMed=6299580;

RA Takeya T., Hanafusa H.;

RT "Structure and sequence of the cellular gene homologous to the RSV src gene and the mechanism for generating the transforming virus.";
Cell 32:881-890(1983).

RL [2]

RP REVISION TO 525.

RA Takeya T., Hanafusa H.;

RL Cell 34:319-319(1983).

RN [3]

RP SEQUENCE FROM N.A., AND PHOSPHORYLATION OF TYR-415 AND TYR-435.

RX MEDLINE=97008971; PubMed=8856081;

RA Weijland A., Neubauer G., Courtneidge S.A., Mann M., Wierenga R.K.,
Superti-Furga G.;

RT "The purification and characterization of the catalytic domain of src expressed in schizosaccharomyces pombe. Comparison of c-
unphosphorylated and tyrosine phosphorylated species.";
Eur. J. Biochem. 240:756-764(1996).

RN [4]

RP SEQUENCE OF 1-18 AND 484-533 FROM N.A.

RX MEDLINE=91304109; PubMed=1712905;

RA Doria T., Levy J.B., Kang L., Brugge J.S., Wang L.H.;

RT "Analysis of cDNAs of the proto-oncogene c-src: heterogeneity in 5'
exons and possible mechanism for the genesis of the 3' end of
v-src.";
J. Cell. Biol. 11:4165-4176(1991).

RN [5]

RP ATP-BINDING SITE.

RX MEDLINE=84270751; PubMed=6431300;

RA Kampf M.P., Taylor S.S., Sefton B.M.,
RT "Direct evidence that oncogenic tyrosine kinases and cyclic AMP-
dependent protein kinase have homologous ATP-binding sites.";
Nature 310:589-592(1984).

RN [6]

RP PHOSPHORYLATION.

RX MEDLINE=86028181; PubMed=2996780;

RA Gould K.L., Woodgett J.R., Cooper J.A., Buss J.E., Shalloway D.,
RA Hunter T.,
RT "Protein kinase C phosphorylates pp60src at a novel site.";
Cell 42:849-857(1985).

RN [7]

RP PHOSPHORYLATION OF TYR-415.

RX MEDLINE=82082387; PubMed=6213838;

RA Smart J.E., Oppermann H., Czernilofsky A.P., Purchio A.F.,
Erikson R.L., Bishop J.M.,
Cell 42:849-857(1985).

RN [8]

RT "Characterization of sites for tyrosine phosphorylation in the transforming protein f Rous sarcoma virus (pp60c-src) and its normal cellular homologue (pp60c-src).";
Proc. Natl. Acad. Sci. U.S.A. 78:6013-6017(1981).

RN PHOSPHORYLATION OF TYR-526.

RX MEDLINE=86151652; PubMed=2420005;

RX

RA Cooper J.A., Gould K.L., Cartwright C.A., Hunter T.;
RT "Tyr27 is phosphorylated in pp60c-src: implications for regulation.";
RN Science 231:1431-1434(1986).

[9]

RP X-RAY CRYSTALLOGRAPHY (2.35 ANGSTROMS) OF 82-532.

RX MEDLINE=9807614; PubMed=9405157;

RA Williams J.C., Weijland A., Gonfoni S., Thompson A.,
Courtneidge S.A., Superti-Furga G., Wierenga R.K.;

RT "The 2.35 Å crystal structure of the inactivated form of chicken src: a dynamic molecule with multiple regulatory interactions.";
J. Mol. Biol. 274:757-775(1997).

RX [10]

RP STRUCTURE BY NMR OF 80-139.

RX MEDLINE=93279385; PubMed=8504863;

RA Yu H., Rosen M.K., Schreiber S.L.;

RT "1H and 15N assignments and secondary structure of the src SH3 domain.";
FEMS Lett. 324:87-92(1993).

RN [11]

RP STRUCTURE BY NMR OF 76-139.

RX MEDLINE=95063992; PubMed=7526465;

RA Feng S., Chen J.K., Yu H., Simon J.A., Schreiber S.L.;

RT "Two binding orientations for peptides to the src SH3 domain: development of a general model for SH3-ligand interactions.";
Science 265:1241-1247(1994).

RX [12]

RP FUNCTION: THE FUNCTION OF PP60-C-SRC IS UNKNOWN. IT IS EXPRESSED IN HIGH LEVELS, AND WITH A HIGH DEGREE OF KINASE ACTIVITY, IN CERTAIN FULLY DIFFERENTIATED CELLS SUCH AS NEURONS, PLATELETS AND MACROPHAGES.

CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein tyrosine phosphate.

CC -!- ENZYME REGULATION: BECOMES ACTIVATED WHEN ITS MAJOR TYROSINE PHOSPHORYLATION SITE IS NOT PHOSPHORYLATED. IT CAN ALSO BE ACTIVATED BY POINT MUTATIONS AS WELL AS BY TRUNCATIONS AT THE C-TERMINAL END OR BY OTHER MUTATIONS.

CC -!- PIM: Phosphorylated on TYR-526 by c-src kinase (CSK). The phosphorylated tail interacts with the SH2 domain thereby repressing kinase activity (By similarity).

CC -!- MISCELLANEOUS: POLYOMA VIRUS MIDDLE T ANTIGEN FORMS A COMPLEX WITH PP60-C-SRC.

CC -!- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. SRC SUBFAMILY.

CC -!- SIMILARITY: Contains 1 SH2 domain.

CC -!- SIMILARITY: Contains 1 SH3 domain.

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CC

DR EMBL; V00402; CAA23696.1; -

DR EMBL; J00844; AAB19353.2; -

DR EMBL; S43604; AAD13831.1; -

DR EMBL; S43616; AAD13835.1; -

DR EMBL; S43587; AAD13830.1; -

DR EMBL; S43609; AAD13832.1; -

DR EMBL; S43614; AAD13834.1; -

DR EMBL; S43579; AAB19353.2; -

DR PIR; A00630; TVCHS.

DR EMBL; S43604; AAD13831.1; -

DR PDB; 1SRM; 31-MAY-94.

DR PDB; 2PTK; 24-DEC-97.

DR PDB; 1PRL; 07-FEB-95.

DR PDB; 1RLP; 07-FEB-95.

DR PDB; 1RLQ; 07-FEB-95.

DR PDB; 1NLO; 27-JAN-97.

DR PDB; 1NLP; 27-JAN-97.

DR PDB; 1F1W; 06-JUL-00.

DR PDB; 1F2F; 06-JUL-00.

DR InterPro; IPR00719; prot_kinase.
 DR InterPro; IPR00880; SH2_.
 DR InterPro; IPR001452; SH3_.
 DR InterPro; IPR001245; Tyr_pk kinase.
 Pfam; PRO0059; kinase; 1.
 Pfam; PRO0017; SH2; 1.
 DR Pfam; PFF00018; SH3; 1.
 DR Prints; PRO00401; SH2DOMAIN.
 DR Prints; PRO00452; SH3DOMAIN.
 DR Prodrom; PRO00109; TYRKINASE.
 DR Prodrom; PRO00001; Prot_kinase; 1.
 DR Prodrom; PD000093; SH2; 1.
 DR Prodrom; PD000066; SH3; 1.
 DR SMART; SM00252; SH2; 1.
 DR SMART; SM0026; SH3; 1.
 DR SMART; SM0019; TYRK; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS0002; SH2; 1.
 KW Tyrosine-protein kinase; Proto-oncogene; Phosphorylation; Transf erase; ATP-binding; Myristate; SH3 domain; SH2 domain; 3D-structure.
 KW INIT_MER 0
 FT LIPID 1
 FT DOMAIN 80
 FT DOMAIN 147
 FT DOMAIN 244
 FT MOD_RES 266
 FT MOD_RES 519
 FT NP_BIND 11
 FT BINDING 272
 FT ACT_SITE 280
 FT ACT_SITE 294
 FT MOD_RES 385
 FT MOD_RES 415
 FT MOD_RES 435
 FT MOD_RES 525
 FT CONFLICT 500
 FT CONFLICT 500
 FT STRAND 84
 FT STRAND 91
 FT STRAND 98
 FT STRAND 101
 FT TURN 103
 FT TURN 104
 FT STRAND 106
 FT STRAND 117
 FT TURN 123
 FT STRAND 125
 FT STRAND 128
 FT HELIX 133
 FT STRAND 135
 FT TURN 136
 FT TURN 139
 FT HELIX 142
 FT TURN 146
 FT STRAND 148
 FT HELIX 154
 FT TURN 162
 FT TURN 168
 FT STRAND 171
 FT TURN 175
 FT STRAND 180
 FT STRAND 183
 FT STRAND 191
 Query Match 27.4%; Score 733; DB 1; Length 532;
 Best Local Similarity 37.9%; Pred. No. 2e-43; Matches 173; Conservative 78; Mismatches 163; Indels 42; Gaps 11;

Qy 66 ELAFRKGVVTEACENKSWYRKHNGSGEGLAAGLAREEALSAQPKLSLMPWFH 125
 98 DLSPRKGERLQLQPPED--GLFLYRESARHPGDWLCVS---FGRDVHYRVLHGD-GH 177
 Qy 126 KISGQEAQVQLQPPED--GLFLYRESARHPGDWLCVS---FGRDVHYRVLHGD-GH 177
 Db 151 KITRRESEPLLNPENPRTGFLYRESEETGAVCLSYSEFDNAKGLAVKHYKIRKLGG 210

Qy 178 LTIDEAVFCNIMDMVBEYSKOKGATKTL--VRPKKKGKRSAEELARAGWLLNQHL 235
 DR 211 FYITSRTOFSSLQOLAVYKHDGCHRLTNCPTSKPQTG---LAKDAWEIPRESL 266
 Db 236 TLGAQIGEGERGAVLGEVLG-OKVAVKNK-CDVTFQAFQLETAWTKMHOENLYRLG 293
 DR 267 RLEVVKLGQGCFGFWMMGFTWNGT"TRVAKTKLKGFTMSAEFLQEAQVKKLREKLUYLA 326
 DR 294 VTHHQGLYTIVMEHVSKGNLVNFRTGRALVNTAQQLQFSLWVAEGMEYLESSKKLHRLD 353
 DR 327 VVSEEPKVIVTEMSKGSLDFLGEMCKYLRLPQLDMAQIASKMAYVERMVYHDL 386
 Qy 354 AARNILVSEDLVAKVSPRGLAKA---ERKGLDSSRPAVKWTAPEALKHGKRTSKDW 409
 DR 387 RAANILVGENLYVKAQDGLARLIEDNEYTAROGAKFKPKIWPAAALYGRTEKSDW 446
 Qy 410 FGULLWEFSYGRAPPKPRMSLKEVSEAVEKGRMRPEFGCPQPVHUMSSCWEAPRR 469
 DR 447 FGILLTELTTKGRVPPGCMVNREBVLQDVERGYRMPCCPPECPSLHDLMCQCWRKDPBEP 506
 Qy 470 PFKLAKIARELRSAGAPASVSGQDADGSTSPRSQ 505
 Db 507 TFPYIQAFL-----EDYFTISTERPQYQ 527.

RESULT 15
 SRC_AVISR
 ID SRC_AVISR STANDARD PRT; 526 AA.
 AC P00525;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 RX 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Tyrosine-protein kinase transforming protein SRC (EC 2.7.1.112) (P60-
 DE SRC).
 OS Avian sarcoma virus (strain rASV141).
 OC Viruses; Retroviridae; Avian type C retroviruses.
 OC NCBI_TaxID=11894;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA M83059858; PubMed=6292477;
 RX Takeya T., Feldman R.A., Hanafusa H.;
 RT "DNA sequence of the viral and cellular src gene of chickens. 1. Complete nucleotide sequence of an EcorI fragment of recovered avian sarcoma virus which codes for gp37 and pp60src.";
 RL J. Virol. 44:1-11(1982).
 RN [2]
 RP PHOSPHORYLATION OF TYR-416.
 RX MEDLINE=81220979; PubMed=6264320;
 RA Neill J.C., Ghysdael J., Vogt P.K., Smart J.E.;
 RT "Homologous tyrosine phosphorylation sites in transformation-specific gene products of distinct avian sarcoma viruses.";
 RT Nature 291:675-677(1981).
 CC -1- FUNCTION: THIS PHOSPHOPROTEIN, REQUIRED FOR BOTH THE INITIATION AND THE MAINTENANCE OF NEOPLASTIC TRANSFORMATION, IS A PROTEIN KINASE THAT CATALYZES THE PHOSPHORYLATION OF TYROSINE RESIDUES
 CC IN VITRO.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC -1- tyrosine phosphatase.
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. SRC
 CC -1- SUBFAMILY.
 CC -1- SIMILARITY: Contains 1 SH2 domain.

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 CC EMBL; R00928; AAA42565.1; -.

DR PDB; 1QWE; 08-MAR-96 .

Job time : 19 secs

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GenCore version 5.1.6
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OM protein - protein search, using SW model.

Run on: July 29, 2003, 09:48:37 ; Search time 44 Seconds

(without alignments)
2973.470 Million cell updates/sec

Title: US-09-977-261-2

Perfect score: 2671

Sequence: 1 MAGRGSLLVSWRAFHCDSAE.....PASVSGQDADGSTSFRSQEP 507

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTRIMBL 23:*

1: SP-archaea:*

2: SP-bacteria:*

3: SP-fungi:*

4: SP-human:*

5: SP-invertebrate:*

6: SP-mammal:*

7: SP-mhc:*

8: SP-organelle:*

9: SP-phage:*

10: SP-plant:*

11: SP-rodent:*

12: SP-virus:*

13: SP-vertebrate:*

14: SP-unclassified:*

15: SP-virus:*

16: SP-bacteriip:*

17: SP-archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

RESULT 1		ALIGNMENTS	
ID	Q9NST8	PRR;	523 AA.
AC	Q9NST8;	PRELIMINARY;	
DT	01-OCT-2000	(TREMBL; 15, Created)	
DT	01-OCT-2000	(TREMBL; 15, last sequence update)	
DT	01-MAR-2003	(TREMBL; 23, Last annotation update)	
DE	Hypothetical protein (Fragment).		
GN	DKF2P43N1212.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
NCBITLEXID	NCBITLEXID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	Tissue=Testis;		
RA	Duesterhoeft A., Lauber J., Mewes H.-W., Weil B., Wiemann S.;		
RL	Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.		
CC	-1 - SIMILARITY: CONTAINS 1 SH3 DOMAIN.		
DR	EMBL: ALJ37754; CAB709061; -.		
DR	HSSP; P11362; IFGK.		
DR	InterPro; IPR000719; Prot_kinase.		
DR	InterPro; IPR000980; SH2.		
DR	InterPro; IPR001452; SH3.		
DR	InterPro; IPR001245; Tyr_Pkinase.		
DR	Pfam; PF00069; Pkinase; 1.		
DR	Pfam; PF00017; SH2; 1.		
DR	Pfam; PF00018; SH3; 1.		
DR	PRINTS; PRO0041; SH2DOMAIN.		
DR	PRINTS; PRO0109; TYRINASE.		
DR	ProDom; PD000001; Prot_kinase; 1.		
DR	ProDom; PD000093; SH2; 1.		
DR	SMART; SM00252; SH2; 1.		
DR	SMART; SM00326; SH3; 1.		
DR	SMART; SM00219; TYRK; 1.		
DR	PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.		
DR	PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.		
DR	PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.		
DR	PROSITE; PS50001; SH2; 1.		

DR	PROSITE: PS0002; SH3; 1; Hypothetical protein; ATP-binding; Kinase; SH3 domain; Transferase; Tyrosine-protein Kinase.
KW	
FT	SEQUENCE 523 AA; 5776 MW; C246280FD7890AFE CRC64;
SO	
Query Match 95.2%; Score 2544; DB 4; Length 523;	Best Local Similarity 96.4%; Pred. No 3.7e-198; Matches 488; Conservative 96.1%; Mismatches 5; Indels 12; Gaps 1; SMART; SNO052; SH2; 1.
Qy 2 AGRCGLSVSRRAFHGCGDSABELPRLVSPRLURAWHPPVSARMPPRRWAPGTCITKCETR 30 AGRG-----SGAPPEQVSPRLRAWHPPVSARMPTTRWAPGTCITKCETR 77	DR SMART; SNO0326; SH3; 1.
Qy 62 PKGELAFLRKGDWVTLACENKSWYRKHTSQEGLLAAGALREREALSLADPKLSMP 121 78 PKGELAFLRKGDWVTLACENKSWYRKHTSQEGLLAAGALREREALSLADPKLSMP 137	DR SMART; SNO0219; TYRK; 1.
Db 122 WFGKRSQEAQVQOLQPPEDGLFVRESARHPPGVYVLCVSGFRVTHYRVLHRQHLD 181 138 WFGKRSQEAQVQOLQPPEDGLFVRESARHPPGVYVLCVSGFRVTHYRVLHRQHLD 197	DR PROSITE; PS50019; PROTEIN_KINASE_TIR; 1.
Qy 182 EAFFFCNLMDMVEYNSKRGAICTKLVPRKRKGTSKSAEELARGWLNLQHLLGQI 241 198 EAFFFCNLMDMVEYNSKRGAICTKLVPRKRKGTSKSAEELARGWLNLQHLLGQI 257	DR PROSITE; PS50001; SH3; 1.
Qy 242 GEFFGAVLQGEVYIGQKAVKVNKIDVTAQAFDDETAVTMKQHENVLQLGVHLHQGLY 301 258 GEFFGAVLQGEVYIGQKAVKVNKIDVTAQAFDDETAVTMKQHENVLQLGVHLHQGLY 317	DR PROSITE; PS50002; SH3; 1.
Db 302 IVMEHNSKGNLVNLTRGRALVTAQOLQFSLVAEGEYEL5SKVHLRDAARNILS 361 318 IVMEHNSKGNLVNLTRGRALVTAQOLQFSLVAEGEYEL5SKVHLRDAARNILS 377	DR ATP-binding; Kinase; SH3 domain; Transferase; Tyrosine-protein Kinase.
Qy 362 EDLVAKVSDFGLAKAERKGKDSSRLPVKWTPEAKLHKFTSKSDVWSRGVLUWEVFSY 421 378 EDLVAKVSDFGLAKAERKGKDSSRLPVKWTPEAKLHKFTSKSDVWSRGVLUWEVFSY 437	DR SEQUENCE 465 AA; 51908 MW; 504B4E8078320C35 CRC64;
Db 422 RAPYKPKMSLKEVSEKEVYMRMEPPGCPGVHMLSSCWEAEPARRPPEPKLAKLARE 481 438 RAPYKPKMSLKEVSEKEVYMRMEPPGCPGVHMLSSCWEAEPARRPPEPKLAKLARE 497	DR SMART; SNO0219; TYRK; 1.
Qy 482 LRGAGAPASVGDAGSTSRSQEP 507 498 LRGAGAPASVGDAGSTSRSQEP 523	DR PROSITE; PS50019; PROTEIN_KINASE_TIR; 1.
RESULT 2	
ID 06176 PRELIMINARY; PRM; 465 AA.	DR SMART; SNO0219; TYRK; 1.
AC Q6176; DT 01-NOV-1996 (TREMBLrel. 01, Created)	DR SMART; SNO0219; TYRK; 1.
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)	DR SMART; SNO0219; TYRK; 1.
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)	DR SMART; SNO0219; TYRK; 1.
DE LSK protein.	DR SMART; SNO0219; TYRK; 1.
GN LSK.	DR SMART; SNO0219; TYRK; 1.
OS Homo sapiens (Human).	DR SMART; SNO0219; TYRK; 1.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	DR SMART; SNO0219; TYRK; 1.
OX NBBI-TAXID=9606; RN [1]	DR SMART; SNO0219; TYRK; 1.
RP SEQUENCE FROM N.A. MEDLINE-9426884; PubMed=7516063; RA McVicar D.W., Lal B.K., Lloyd A., Kawamura M., Chen Y.Q., Zhang X., Staples J.E., Ortaldo J.R., O'Shea J.J.; RT "Molecular cloning of lsk, a carboxy-terminal src kinase (csk) related gene, expressed in leukocytes"; DR Oncogene 9;2037-2044(1994).	DR SMART; SNO0219; TYRK; 1.
CC -1 SIMILARITY: CONTAINS 1 SH3 DOMAIN. EMBL: S71669; AAB30995.1; DR HSSP: P11362; IFGK InterPro: IPR000719; PICT_kinase. InterPro: IPR000380; SR2.	DR SMART; SNO0219; TYRK; 1.
RESULT 3	
ID 064103 PRELIMINARY; PRT; 511 AA.	DR SMART; SNO0219; TYRK; 1.
AC Q64103; DT 01-NOV-1996 (TREMBLrel. 01, Created)	DR SMART; SNO0219; TYRK; 1.
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)	DR SMART; SNO0219; TYRK; 1.
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)	DR SMART; SNO0219; TYRK; 1.
DE VNK protein.	DR SMART; SNO0219; TYRK; 1.
OS Mus sp.	DR SMART; SNO0219; TYRK; 1.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	DR SMART; SNO0219; TYRK; 1.
OX NCBI-TAXID=10095; RN [1]	DR SMART; SNO0219; TYRK; 1.
RP SEQUENCE FROM N.A. MEDLINE-95178994; PubMed=7874011; RA Ersler M.A., Kriktsov A.V., Krotkova A.V., Beliavskii A.V., RA Visser J.V.; RT "Vnk-a new gene for nonreceptor protein-tyrosine kinase, expressed	DR SMART; SNO0219; TYRK; 1.

QY	222 ELARAGWLNLNQHILTLGAQIGEGERGAVIQLQGEYLQKVKAVKNIKCDVTAQAFDETAVMT	281	QY	42 MPTRRWAPGTOCTTKCEHTRPKPGELAFRKGDVUTLACEENKSWYRKHTSGQEGILA	101
Db	180 ELARAGWLNLQHILTLGAQIGEGERGAVIQLQGEYLQKVKAVKNIKCDVTAQAFDETAVMT	239	Db	1 MPT-RWAPGTOCTTKCEHTRPKPGELAFRKGDVUTLACEEDKSWYRAKHGSQEGILA	59
QY	282 KMQHENLVRLIGVTLHQGLYIVMHRVSKQNLVNFLTRGRALYVTAQLOFSLIVAEQE	341	QY	102 AGALRREALSAPPKLSPMPLWFGKIKSQEAOVQOLPREGDGLVRESARHGDYVLCVS	161
Db	240 KLOHRLNLVRLIGVTLHQGLYIVMHRVSKQNLVNFLTRGRALYVTAQLOFSLIVAEQE	299	Db	60 RAALRQREALSTDPEKLSLMPWFHGKISQEAQOLQPPEDGLFLVRESARHGDYVLCVS	119
QY	342 YLESKVLVRLDAARNLIVSLEDYAVKSFGLAKAERKLDSSRLPVKTAPEALKHGF	401	QY	162 FGROVTHYVLRLIGVTLHQGLYIVMHRVSKQNLVNFLTRGRALYVTAQLOFSLIVAEQE	221
Db	300 YLESKVLVRLDAARNLIVSLEDYAVKSFGLAKAERKLDSSRLPVKTAPEALKHGF	359	Db	120 FGROVTHYVLRLIGVTLHQGLYIVMHRVSKQNLVNFLTRGRALYVTAQLOFSLIVAEQE	179
RESULT 5			QY	222 ELARAGWLNLNQHILTLGAQIGEGERGAVIQLQGEYLQKVKAVKNIKCDVTAQAFDETAVMT	281
P77223	SEQUENCE FROM N.A.	PRELIMINARY;	PRT;	465 AA.	QY
ID	PT0223	PRELIMINARY;	PRT;	465 AA.	Db
AC	01-FEB-1997 (TREMBlrel. 02, Created)				180 ELARAGWLNLQHILTLGAQIGEGERGAVIQLQGEYLQKVKAVKNIKCDVTAQAFDETAVMT
DT	01-FEB-1997 (TREMBlrel. 02, Last sequence update)				239
DT	01-MAR-2003 (TREMBlrel. 23, Last annotation update)				360 SSKSDWWSFGVLLMVEFSGRAPYPKMSIKEVSEAVERGKYMEEPDGPGSVHTLMSGCW
DE	HYL tyrosine kinase.				419
GN	MATK OR HYLTK.				QY
OS	Mus musculus (Mouse).				282 KMQHENLVRLIGVTLHQGLYIVMHRVSKQNLVNFLTRGRALYVTAQLOFSLIVAEQE
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;				341
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				240 KLOHRLNLVRLIGVTLHQGLYIVMHRVSKQNLVNFLTRGRALYVTAQLOFSLIVAEQE
RN	[1]				299
RP	SEQUENCE FROM N.A.				QY
RC	STRAIN=CBX C57BL/6; TISSUE=Embryonic stem;				402 TSKSDWWSFGVLLMVEFSGRAPYPKMSIKEVSEAVERGKYMEEPDGPGSVHTLMSGCW
RX	MEDLINE=96280730; Pubmed=864808;				461
RA	Hamaguchi I., Yamaguchi N., Suda J., Hirac A., Hashiyama M.,				Db
RA	Aizawa S.I., Suda T.,				360 SSKSDWWSFGVLLMVEFSGRAPYPKMSIKEVSEAVERGKYMEEPDGPGSVHTLMSGCW
RT	*Analysis of CSK homologous kinase (CSK/HYL) in hematopoiesis by				419
RT	utilizing gene knockout mice.;				QY
RL	Blochim. Biophys. Res. Commun. 224:172-179(1996).				462 EAEPARRPFPKLAELRSLRSGAPASVSGODAGSTSAPRSQEP 507
CC	-1 SIMILARITY: CONTAINS 1 SH3 DOMAIN.				Db
DR	EMBL: X33972; CAAS8806.1; -.				420 EAEPARRPFPKLAELRSLRSGAPASVSGODAGSTSAPRSQDP 465
DR	MGD: MGI-9959; Matk.				
DR	InterPro; IPR00719; Prot_kinase.				
DR	InterPro; IPR00980; SH2.				
DR	InterPro; IPR01452; SH3.				
DR	InterPro; IPR00125; Tyr_pk kinase.				
DR	Pfam; PF00069; pk kinase; 1.				
DR	Pfam; PF1362; IFGK.				
DR	Pfam; PF00017; SH2; 1.				
DR	Pfam; PF00018; SH3; 1.				
DR	PRINTS; PR00041; SH2DOMAIN.				
DR	PRINTS; PR00109; TYRKINASE.				
DR	PRODom; PD000001; PROT_kinase; 1.				
DR	PRODom; PD000093; SH2; 1.				
DR	SMART; SM0052; SH2; 1.				
DR	SMART; SM00326; SH3; 1.				
DR	SMART; SM00329; SH3; 1.				
DR	PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.				
DR	PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.				
DR	PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.				
DR	PROSITE; PS50001; SH2; 1.				
DR	PROSITE; PS50002; SH3; 1.				
DR	ATP-binding; Kinase; SH3 domain; Transferase; Tyrosine-protein kinase.				
SQ	SEQUENCE 465 AA; 51571 MW; 24C2DBA71A08A3E9 CRC64;				
Query Match	Best local Similarity 82.9%; Score 2214.5; DB 11; Length 465;				
Matches	417; Conservative 24; Mismatches 24; Indels 1; Gaps 1;				

RESULT	9
Q9VGK8	PRELIMINARY; PRT; 723 AA.
ID	Q9VGK8
AC	Q9VGK8; 09VGK9;
DT	01-MAY-2000 (TREMBLrel. 13, Created)
DT	01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DE	CG17309 protein.
GN	CG17309
OS	Drosophila melanogaster (Fruit fly).
OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydriidea; Drosophilidae; Drosophila.
OC	NCBI_TAXID=7227;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=Berkeley; MEDLINE=20196006; PubMed=10731132;
RX	Adams M.D., Celunker S.E., Holt R.A., Evans C.A., Gocayne J.D., Almásiadics P.G., Scheier S.E., Li P.W., Hopkins R.A., Gallo R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Hsiao S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Chamele M., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Heitz G., Nelson C.R., Miklos G.L.G., Abril J.F., Agbayani A., An H.-J., Andrews-Pfankoch C., Baldwin D., Balliew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Beeson K.M., Benos P.V., Bermudez B.P., Bhandari D., Bolisariova S., Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., Burtsis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., Cherry J.M., Cawley S., Danilek C., Davenport L.B., Davies P., de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., Dodson K., Douc L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Dubin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W., Fosler C., Gabrielian A.E., Garg N.S., Geibart W.M., Glasser K., Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J., Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeagwam C., Jalali M., Kalush F., Karpen G.H., Ke Z., Kettunison J.A., Ketchum K.A., Kimmel B.E., Kodlisch F., Karpen H., Ke Z., Kettunison J.A., Ketchum K.A., Klimmel B.E., Kodlisch F., Kraft C., Kravitz S., Kulp D., Lai Z., Lasko P., Lei Y., Levittsky A.A., Li J., Li Z., Liang Y., Lin X., Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D., Merkulov G., Milshina N.V., Mobbyar C., Morris J., Moskrafi A., Mount S.M., Moy M., Murphy B., Murphy L., Muzyz D.M., Nelson D.L., Nelson D.R., Nelson K.A., Nixon K., Nusslein D.R., Pacleb J.M., Palazzotto M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., Spier E., Spadring A.C., Stapleton M., Strong R., Sun E., Svirkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C., RT "the genome sequence of Drosophila melanogaster.", Science 287:2185-2195(2000).
RN	[2]
RP	SEQUENCE FROM N.A.
RA	Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y., Celunker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A., Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A., Carlson J.W., Center A., Champé M., Davenport L.B., Dietz S.M., Dodson K., Dorsett V., Douc L.E., Doyle C., Dresen D., Farfan D., Ferriera S., Frise E., Gallo R.F., Garg N.S., George R.A., Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howard T.J., Ingwam C., Jalali M., Kruse D., Li P., Mattei B., Moskrafi A., Mcintosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nuno J., Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B., Phoumenavong S., Pitman G.S., Pui V., Richards S., Scheeler F., Stapleton M., Strong R., Svirkas R., Tector C., Tyler D., Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
RA	"sequencing of Drosophila melanogaster genome".

PFam; PF00018; SH3; 1.	RT	"Two new isoforms of v-Src oncogene isolated from low and high
DR	RT	metastatic RSV-transformed hamster cells.;"
PRINTS; PRO0041; SH2DOMAIN.	RL	Virology 216:347-356 (1995).
PRINTS; PRO0109; TYRKINASE.	CC	!-SIMILARITY: CONAINS 1 SH3 DOMAIN.
DR	DR	EMLB: X84074; CAA5B881.1; -.
PRODom; PD000093; SH2; 1.	DR	HSSP: P00524; ISPR
DR	DR	InterPro; IPR000719; Prot_kinase.
PRODom; PD000066; SH3; 1.	DR	InterPro; IPR000980; SH2.
DR	DR	InterPro; IPR001452; SH3.
SMART; SM00219; TYRK; 1.	DR	InterPro; IPR001245; Tyr_Pkinase.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.	DR	Pfam; PF00069; pkine; 1.
DR	DR	PROSITE; PS00109; PROTEIN_KINASE_TIR; 1.
PROSITE; PS50001; SH2; 1.	DR	PROSITE; PS50002; SH3; 1.
DR	DR	PROSITE; PS50001; SH2; 1.
ATP-binding; Kinase; SH3 domain; Transferase; Tyrosine-protein kinase.	DR	PROSITE; PS50002; SH3; 1.
SEQUENCE 509 AA; 57946 MW; FIBREFC237C8DB7E CRC64; SQ	DR	PROSITE; PS50001; SH2; 1.
Query Match 27.6%; Score 737.5; DB 6; Length 509; Best Local Similarity 37.4%; Pred. No. 2.5e-51; Matches 160; Conservative 87; Mismatches 156; Indels 25; Gaps 9; Scores 310	DR	PRINTS; PRO00452; SH2DOMAIN.
QY 65 GELARPKGDVVTILEAACENSKSWYRKHHTSGQEGGLIAAGALRERALSADPKLSMPWFH 124	DR	PRINTS; PRO00109; TYRKINASE.
Db 78 GDLGFEKGEORLIE--QSEWWKQSLTGQEGEITPFNIVAKANSLPE-----PWFF 129	DR	PRODom; PD000001; Prot_kinase; 1.
QY 125 GKISQEQAEVQOLQPPED--GLFLYRESARHPGDVYLCV-----SGRDVHYRVLHRD-G 176	DR	PRODom; PD000093; SH2; 1.
Db 130 KNLSRKDAEROLLAGNTHGSFLRESESTAGSFSLSVRDFDONGEUVKHYKTRNLNG 189	DR	PRODom; PD000001; Prot_kinase; 1.
QY 177 HLTDIEAVFCNLMDMVEHYSKDKGAIKCKLVRVPRKHGTSAEELARAGWLLNLQHLT 236	DR	PRODom; PD000066; SH3; 1.
Db 190 GFYIISPRITPGLHLILVRYTNASGLCTRLSPQO--TQKPOKPWEDEWVIRETLK 246	DR	SMART; SM00252; SH2; 1.
QY 237 LGAQTCGEGERGAVLQGEGYLGQ-KVAVKNIK-CDVTAQAFDLETAVMTKHOHENLYVRLLG 294	DR	SMART; SM00219; TYRK; 1.
Db 247 LVERLIGAGORGEVWMMGYYNQHTKAVKSLKQGSMSPDADFLAEANILMKOHLRVLRYAV 306	DR	PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
QY 295 ILHQQLYTMEHVSKGNLNVFLRTRGRALVNTAQQLQFSLHVAEQMEYLESKKLVHRDLA 354	DR	PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
Db 307 VTQEPIYVITEYMEGNSVLDFLKAPSGIKLTINKLIDMAQIAEGMAFERNYIHDRLR 366	DR	PROSITE; PS50010; PROTEIN_KINASE_TIR; 1.
QY 355 ARNIVLSEDLVYKVSDFGLAKA---ERKGLDSSILPVKVTAAPEALKHGFTSKSDVWSF 410	DR	PROSITE; PS50001; SH2; 1.
Db 367 AANLIVSITDUSLICKIAFLGARLIELDEYTAREGAFPIKTMIAPEINYGFTIKSDVWSF 426	DR	PROSITE; PS50002; SH3; 1.
QY 411 GVLWLEVFVSYGRAPYKPKMSLKEVSKRVEKSYRMEPEGCQGPVHVTMSSWEEAARRPP 470	DR	ATP-binding; Kinase; SH3 domain; Transferase; Tyrosine-protein kinase.
Db 427 GILETEIVTHGRIKPPGPMNTPVQNLERFIRMPDNPNEELKQMLMQLWERDERDRPT 486	DR	SEQUENCE 545 AA; 61037 MW; 4C4E34BC75266913 CRC64; SQ
QY 471 FRKLAELK 478	DR	Query Match 27.6%; Score 736; DB 15; Length 545; Best Local Similarity 35.6%; Pred. No. 3.7e-51; Matches 187; Conservative 82; Mismatches 181; Indels 76; Gaps 16; Scores 310
Db 487 FDYLRSVL 494	DR	QY 14 HCDSABELP-----VSPRFLRAWHPP-----PVSARMTRWAPGT----- 51
QY 26 HEGFPASQTPNPKTAPLTAAPRSSR--RPPASOHRRAAPDTHTPSPRSF--GIVANERKLP 81	DR	Db 52 -----OCITKCEHTRPKG-----ELAERKGVDVVTILEACENSWYR 88
Db 82 GDFNTSDTPTSPORARTFLAGVITFVALYDVSWEITDLSFKRGERLQIVNNTG-NWWL 140	DR	Db 89 VVHHTISQEGGLIAAGALRERERALSADPKLSMPWFHKGKISGQEAQVOLQPPED--GLFLV 146
QY 141 AHSVTGQTGQYIPSNVAPPSQIPE-----EWYCKITRRESGRILNPINPRGFV 194	DR	Db 141 RHSVTGQTGQYIPSNVAPPSQIPE-----EWYCKITRRESGRILNPINPRGFV 194
Db 147 RESARHPGDDYVICS----FGRDVLHYRVLHD-GHILTDIEAVFCNLMDMVEHYSKDK 200	DR	Db 147 RESARHPGDDYVICS----FGRDVLHYRVLHD-GHILTDIEAVFCNLMDMVEHYSKDK 200
QY 195 RESETTKGAYCILSVSDEDNAKGLENVKHYKIRKLDSGGFYIISRTQFSSLQQLVAYSKHA 254	DR	Db 201 GAICTKL--VPRKRHGTSKAEEELARAGWLNQHLTGQIGESEFGAVIQLQEGYLG-Q 257
Db 255 DGLCHRHTNVCPTSKPOTQG---LAKDAWEIPRESLRLEVKGQGCFGEVNGTNGTT 310	DR	Db 255 DGLCHRHTNVCPTSKPOTQG---LAKDAWEIPRESLRLEVKGQGCFGEVNGTNGTT 310
QY 258 KVAVKNIK-CDVTAQAFDLETAVMTKHOHENLYVRLGVILHQLYIWEHVSKGNLNVFL 316	DR	Db 311 RYAIKTLKPGTMSPEAFQLQEVQMKLKRHEKJLVQLYAVSERPIVIVYEVSKGSLLNLF 370
Db 317 RYRGRALVNTAQQLQFSLHVAEQMEYLESKKLVHRDLAARNITLVEDLVAQVSKDFGLAKA 376	DR	Db 317 RYRGRALVNTAQQLQFSLHVAEQMEYLESKKLVHRDLAARNITLVEDLVAQVSKDFGLAKA 376
QY 371 KGEMGKVLRPQLPQVDMQAQISGMMAYVERMMVHVRDIAANITLVGELECKVADFGGLR 430	DR	Db 371 KGEMGKVLRPQLPQVDMQAQISGMMAYVERMMVHVRDIAANITLVGELECKVADFGGLR 430
DE P624v.	DR	QY 377 ---ERKGLDSSILPVKVTAAPEALKHGFTSKDWSFGVLIWEVFSYGRAPYKPKMSLKE 432
GN SRLM.	DR	Db 431 TEDNEYTAQGKPAKWTAAPEAGLGRFTKSDWSFGVLIWELTETKGRGPYPGMNGE 490
OS Rous sarcoma virus.	DR	QY 433 VSEAVEVKYRMEPEPGCGPVGIVLMSMSCWEAEPARRDPFRKLAELK 478
OC Viruses; Retroviridae; Retroviridae; Alpharetrovirus.	DR	Db 491 VLDVRVERGYRMPCPPECPESTHDLMCOCWREPEERPTFEVLAQO 536
OX NCBI_TaxID:1886;	DR	Dezeleka P;
RN [1]	DR	RP SEQUENCE FROM N.A.
RP MEDLINE:96183936; PubMed=8607264;	DR	RX Tatsosyan A., Yatsula B., Shtrutman M., Moinova E., Kaverina I., Musatina E., Leskov K., Mizenina O., Zueva E., Galothe G., Musatina E., Leskov K., Mizenina O., Zueva E., Galothe G., Dezeleka P;

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